



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 100977**

**TO: Elizabeth Kemmerer**  
**Location: CM1/10B17/10D19**  
**Art Unit: 1646**  
**Tuesday, August 19, 2003**  
**Case Serial Number: 09581252**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**CM1-6B06**  
**Phone: 305-1954**

**[paul.schulwitz@uspto.gov](mailto:paul.schulwitz@uspto.gov)**

### **Search Notes**

Examiner Kemmerer,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(703)305-1954



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 14:30:54 ; Search time 83 Seconds

(without alignments)  
675.066 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848  
Sequence: 1 MNECHYKHMDFYNNRSTMD.....GSQYIEDISOGAVCNKSTS 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Minimum number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A.Geneseq\_19Jun03:\*

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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15: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
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23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1848	100.0	353	20	AAV24240
2	1838	99.5	353	20	AAV24241
3	1838	99.5	353	21	AAV24242
4	1838	99.5	353	21	AAV24243
5	1838	99.5	353	22	AAV24244
6	1838	99.5	353	23	AAV24245
7	1838	99.5	353	23	AAV24246
8	1838	99.5	353	24	AAV24247
9	1838	99.5	353	24	AAV24248

10	1838	99.5	353	24	AB056733
11	1838	99.5	353	20	AB081689
12	1834	99.2	353	20	AAV24242
13	1775	96.0	353	24	ABP56225
14	1772.5	95.9	354	21	AAV24243
15	1697.5	91.9	354	24	ABP56224
16	1692.5	91.6	354	24	AAV24243
17	1692.5	91.6	354	21	AAV24243
18	1692.5	91.6	354	23	ABP7818
19	1682.5	91.0	354	24	ABP56226
20	1642.5	88.9	345	24	ABP56227
21	1546	83.7	338	19	AAV24244
22	1014.5	54.9	220	22	AAV24244
23	995	53.8	213	10	AAV24244
24	948.5	51.3	364	18	AAV24244
25	948.5	51.3	364	20	AAV24244
26	948.5	51.3	364	22	AAV24244
27	948.5	51.3	364	22	AAV24244
28	948.5	51.3	364	24	ABP56228
29	948.5	51.3	364	24	ABP56228
30	948.5	51.3	364	24	ABP56228
31	946.5	51.2	364	19	AAV24244
32	946.5	51.2	364	19	AAV24244
33	946.5	51.2	364	20	AAV24244
34	946.5	51.2	364	20	AAV24244
35	944.5	51.1	364	18	AAV24244
36	853.5	46.2	351	20	AAV24244
37	849.5	46.0	348	23	ABP56229
38	849.5	46.0	382	20	AAV24244
39	849.5	46.0	382	21	AAV24244
40	849.5	46.0	382	22	AAV24244
41	849.5	46.0	382	24	ABP56229
42	849.5	46.0	382	24	ABP56229
43	843.5	45.6	351	19	AAV24244
44	843.5	45.6	351	21	AAV24244
45	843.5	45.6	351	23	AAV24244

#### ALIGNMENTS

RESULT 1	AAV24240	standard; Protein; 353 AA.
XX	AAV24240;	
AC	13-SEP-1999	(first entry)
XX		
DT	Human EDG-5 receptor.	
XX		
DE	Human EDG-5 receptor.	
XX		
KW	EDG-5; HEDG-5; MEND-5; receptor homologue; asthma; rheumatoid arthritis;	
KW	adult respiratory distress syndrome; cardiac ischaemia; septic shock;	
KW	acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;	
KW	early diabetic glomerulopathy; lung damage.	
OS	Homo sapiens.	
XX		
PN	WO933972-A1.	
XX		
PD	08-JUL-1999.	
XX		
PF	24-DEC-1998; 98WO-CA01193.	
XX		
PR	24-DEC-1997; 97US-0997803.	
XX		
PA	(ALIX ) ALLELIX BIOPHARMACEUTICALS INC.	
XX		
PI	Chun JW, Gupta AK, Munroe DG, Vyas TB;	
XX		
DR	WPI; 1999-419106/35.	
DR	N-PSDB; AAX8745.	
XX		

Lung cancer-associ  
Human lysophosphat  
Human EDG-5 recept  
Human EDG7 recepto  
Human HOFNH30 prot  
Rat EDG7 receptor  
Murine EDG-5 recep  
Murine G protein-c  
Amino acid sequenc  
Mouse EDG7 recepto  
Rat G protein-coupl  
HOFNH30 polypeptid  
Human expressed po  
Murine EDG-5 recep  
Human G-protein co  
Human EDG-1 protel  
Human protein sequ  
LPA receptor, EDG-  
Human lysophosphat  
Human Edg2 recepto  
Human lysophosphat  
Rat olfactory bulb  
Rat olfactory bulb  
Murine lysophosphat  
Murine LPA recepto  
Human EDG-2 recept  
Human edg-6 protel  
Mouse 7-transmembr  
Human EDG-4 protel  
Human acid sequenc  
LPA receptor-relat  
Human lysophosphat  
Chimeric human Edg  
Human HEBG90 prot  
Amino acid sequenc  
Human G-protein co

PT Nucleotide sequences encoding mammalian EDG-5 receptors  
XX  
PS Claim 13; Fig 4A; 87pp; English.  
CC The present sequence is a human EDG-5 (HEDG-5) receptor homologue.  
CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5  
CC and can accelerate diagnosis and proper treatment of conditions such as  
CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,  
CC cardiac ischaemia, acute pancreatitis, septic shock, psoriasis, acute  
CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well  
CC as lung damage following exposure to cigarette smoke, asbestos, or  
CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used  
CC to treat inflammation or diseases including, viral, bacterial or fungal  
CC infections, allergic responses, mechanical injury associated with  
CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions  
CC which activate the genes of kidney, lung, heart, lymphoid or tissues of  
CC the nervous system.  
XX  
SQ Sequence 353 AA;  
Query Match 100.0%; Score 1848; DB 20; Length 353;  
Best Local Similarity 100.0%; Pred. No. 2.3e-197;  
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 MNECHYKHMDFEYFRNSNTDTVDWDTGKLYIVLCVGTFFCLFFFSNSLYIAVINKRK 60  
1 MNECHYKHMDFEYFRNSNTDTVDWDTGKLYIVLCVGTFFCLFFFSNSLYIAVINKRK 60  
QY 61 FHFFPYLLANLAADFPAGIAYVFLMFTGPKVSKTTLVNRMTLROGLDSSLTASLTNL 120  
61 FHFFPYLLANLAADFPAGIAYVFLMFTGPKVSKTTLVNRMTLROGLDSSLTASLTNL 120  
DB 121 LVIAVERHMSIMRRVHSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180  
121 LVIAVERHMSIMRRVHSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180  
QY 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240  
181 PIYSRSYLVEWTVSNLMAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240  
DB 241 VMTVLGAFVVCWMTGVLVPLDGLNCRQCGVQVHKRMFLALALNSVYVNPPIIYSYKDEDM 300  
241 VMTVLGAFVVCWMTGVLVPLDGLNCRQCGVQVHKRMFLALALNSVYVNPPIIYSYKDEDM 300  
QY 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
RESULT 2  
ID AAY24241 standard; Protein: 353 AA.  
AC AAY24241;  
DT 13-SEP-1999 (first entry)  
DE Human EDG-5 receptor clone pc3-hedg5#3.4 protein.  
XX  
XX EDG-5; HEDG-5; MEDG-5; receptor homologue; asthma; rheumatoid arthritis;  
KW adult respiratory distress syndrome; cardiac ischaemia; septic shock;  
KW acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;  
KW early diabetic glomerulopathy; lung damage.  
OS Homo sapiens.  
XX  
XX WO9933972-A1.  
XX  
XX 08-JUL-1999.  
XX  
XX 24-DEC-1998; 98WO-CA01193.  
XX  
XX 24-DEC-1997; 97US-0997803.  
PR

XX  
PA (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.  
XX  
XX Chun JYM, Gupta AK, Munroe DG, Vyas TB;  
PI  
XX WPI: 1999-419106/35.  
DR  
XX N-PSDB: AAX86746.  
PT Nucleotide sequences encoding mammalian EDG-5 receptors  
PS Claim 13; Fig 4B; 87pp; English.  
XX  
XX The present sequence is a human EDG-5 (HEDG-5) receptor homologue.  
CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5  
CC and can accelerate diagnosis and proper treatment of conditions such as  
CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,  
CC cardiac ischaemia, acute pancreatitis, septic shock, psoriasis, acute  
CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well  
CC as lung damage following exposure to cigarette smoke, asbestos, or  
CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used  
CC to treat inflammation or diseases including, viral, bacterial or fungal  
CC infections, allergic responses, mechanical injury associated with  
CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions  
CC which activate the genes of kidney, lung, heart, lymphoid or tissues of  
CC the nervous system.  
XX  
SQ Sequence 353 AA;  
Query Match 99.5%; Score 1838; DB 20; Length 353;  
Best Local Similarity 99.7%; Pred. No. 3.1e-196;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
DB 1 MNECHYKHMDFEYFRNSNTDTVDWDTGKLYIVLCVGTFFCLFFFSNSLYIAVINKRK 60  
1 MNECHYKHMDFEYFRNSNTDTVDWDTGKLYIVLCVGTFFCLFFFSNSLYIAVINKRK 60  
QY 61 FHFFPYLLANLAADFPAGIAYVFLMFTGPKVSKTTLVNRMTLROGLDSSLTASLTNL 120  
61 FHFFPYLLANLAADFPAGIAYVFLMFTGPKVSKTTLVNRMTLROGLDSSLTASLTNL 120  
DB 121 LVIAVERHMSIMRRVHSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180  
121 LVIAVERHMSIMRRVHSNLTGKRVTLILLVMAIAIFMGAVPTLGNMCLNISACSSLA 180  
QY 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240  
181 PIYSRSYLVEWTVSNLMAFLIMVYVLRITYYVARKTNVLSPHSGSISRRTPMKLMKT 240  
DB 241 VMTVLGAFVVCWMTGVLVPLDGLNCRQCGVQVHKRMFLALALNSVYVNPPIIYSYKDEDM 300  
241 VMTVLGAFVVCWMTGVLVPLDGLNCRQCGVQVHKRMFLALALNSVYVNPPIIYSYKDEDM 300  
QY 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKKMICPSQENPERRPSRIPSTVLSRSDTSQYIEDSISOGAVCNKSTS 353  
RESULT 3  
ID AAB10098 standard; Protein: 353 AA.  
AC AAB10098;  
DT 10-NOV-2000 (first entry)  
DE Human G protein-coupled receptor hAL7T024.  
XX  
XX G protein-coupled receptor; AL7T024; treatment; prevention; diagnosis;  
KW nervous system disorder; Alzheimer's disease; dementia; hypertension;  
KW inflammatory disorder; allergy; rheumatism; asthma; arteriosclerosis;  
KW cardiovascular disorder; cancer; human.  
OS Homo sapiens.

XX WO200035953-A1.  
XX 22-JUN-2000.  
XX 09-DEC-1999; 99WO-JP06904.  
XX 11-DEC-1998; 98JP-0353165.  
XX 08-FEB-1999; 99JP-0029677.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Watanabe T, Kikuchi K, Shintani Y;  
XX WPI; 2000-442368/38.  
XX N-PSDB; AAA40370.  
XX G-protein coupled receptor protein and antibodies to it for treatment  
XX and diagnosis of nervous system, inflammatory and other disorders  
XX  
XX Claim 2; Page 88-90; 94pp; Japanese.

CC This invention describes a novel G-protein coupled receptor protein  
CC (AL7T024) and its salts. The products of the invention can be used for  
CC the treatment, prevention and diagnosis of diseases with which the  
CC receptor protein is associated, including nervous system disorders (such  
CC as Alzheimer's disease and dementia), inflammatory disorders (such as  
CC allergies, rheumatism and asthma), cardiovascular disorders (such as  
CC hypertension and arteriosclerosis), and cancer. This sequence represents  
CC the human G protein-coupled receptor protein which is described in the  
CC method of the invention.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 21; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYIAVYKRNK 60  
DB 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYIAVYKRNK 60  
QY 61 FHEPPYYLLANLAADFFAGIAYVFLMFTGVSSTLVNRMFLROGLDSSLTASTNL 120  
DB 61 FHEPPYYLLANLAADFFAGIAYVFLMFTGVSSTLVNRMFLROGLDSSLTASTNL 120  
QY 121 LVIAVERHMSIMRMVHNSLTKKRYTLILVMAIAIFMGAVPTLGMNCLCINISACSSIA 180  
DB 121 LVIAVERHMSIMRMVHNSLTKKRYTLILVMAIAIFMGAVPTLGMNCLCINISACSSIA 180  
QY 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRTPKMLKT 240  
DB 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRTPKMLKT 240  
QY 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVYKRMFLLLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVYKRMFLLLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMKMKICCFQSENPERRRPSRIPTSVLSRSDTGSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKMKICCFQSENPERRRPSRIPTSVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 4

AA551227  
ID AAY51227 standard; Protein; 353 AA.

XX AAY51227;

XX 06-APR-2000 (first entry)

XX Human G protein-coupled receptor protein.

XX

KM G protein-coupled receptor; human; lysophosphatidic acid; diagnosis;  
KM treatment; prostate cancer; prostatic hyperplasia; inflammation.

XX Homo sapiens.

XX WO9967383-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-JP03306.

XX 22-JUN-1998; 98JP-0174731.

XX (NISR ) JAPAN TOBACCO INC.

XX Nozaki Y, Naito T;

XX WPI; 2000-106293/09.

XX N-PSDB; AA244359.

XX G-protein coupled receptor protein binding to lysophosphatidic acid  
XX used for treatment of prostate cancer -

XX Claim 1; Page 55-57; 67pp; Japanese.

CC This invention describes a novel human G-protein coupled receptor  
CC protein capable of binding lysophosphatidic acid, and proteins derived  
CC from it by addition, deletion and/or substitution of one or more amino  
CC acid residues. Antibodies to the protein are used for diagnosis of, and  
CC agonists/antagonists to the protein are used for the treatment of,  
CC prostatic disorders such as prostate cancer, benign prostatic  
CC hyperplasia, and inflammation of the prostate. This sequence represents  
CC the human G protein-coupled receptor protein described in the method of  
CC the invention.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 21; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-196;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYIAVYKRNK 60  
DB 1 MNECHYDKHMDFFYRNSNTDVTGKLVYLCVGFECLEFFFSNSLYIAVYKRNK 60  
QY 61 FHEPPYYLLANLAADFFAGIAYVFLMFTGVSSTLVNRMFLROGLDSSLTASTNL 120  
DB 61 FHEPPYYLLANLAADFFAGIAYVFLMFTGVSSTLVNRMFLROGLDSSLTASTNL 120  
QY 121 LVIAVERHMSIMRMVHNSLTKKRYTLILVMAIAIFMGAVPTLGMNCLCINISACSSIA 180  
DB 121 LVIAVERHMSIMRMVHNSLTKKRYTLILVMAIAIFMGAVPTLGMNCLCINISACSSIA 180  
QY 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRTPKMLKT 240  
DB 181 PIYSRSYLVFWTWSNLMFLIMVYVLRIVYVKKRTNVLSPHTSGSISRRTPKMLKT 240  
QY 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVYKRMFLLLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVLGAFVVCWTPGLVYVPLDGLNCRQCGVOHVYKRMFLLLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMKMKICCFQSENPERRRPSRIPTSVLSRSDTGSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKMKICCFQSENPERRRPSRIPTSVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 5

AAE04563  
ID AAE04563 standard; Protein; 353 AA.

XX AAE04563;

XX 04-SEP-2001 (first entry)

XX

XX Human G-protein coupled receptor-19 (GRC-19) protein.  
 DE  
 XX Human G-protein coupled receptor-19; GRC-19; gene therapy; cirrhosis;  
 KW transgenic animal; proliferative disorder; actinic keratosis; hepatitis  
 KW nephrotic; cancer; breast; bladder; bone marrow; brain; uterus;  
 KW leukemia; adenocarcinoma; lymphoma; melanoma; myeloma; epilepsy; stroke;  
 KW neurological disorder; Alzheimer's disease; Parkinson's disease; nausea;  
 KW Huntington's disease; multiple sclerosis; dementia; angina pectoris;  
 KW central nervous system disorder; cardiovascular disorder; hypertension;  
 KW atherosclerosis; congestive heart failure; gastrointestinal disorder;  
 KW dysphagia; peptic esophagitis; spasm; gastritis; anorexia; pyrosis;  
 KW pancreatitis; Crohn's disease; diarrhoea; autoimmune disorder; anaemia;  
 KW inflammatory disorder; Acquired Immune Deficiency Syndrome; AIDS;  
 KW Addison's disease; allergy; asthma; diabetes mellitus; antithyroid;  
 KW atopic dermatitis; glomerulonephritis; Grave's disease; psoriasis;  
 KW rheumatoid arthritis; ulcerative colitis; osteoporosis; antifungal;  
 KW metabolic disorder; obesity; nocturnal; protozoa; virucide.

XX Homo sapiens.  
 FT Key  
 FT Location/Qualifiers  
 FT 36..56  
 FT /label=Transmembrane\_domain  
 FT 146..166  
 FT /label=Transmembrane\_domain  
 FT 187..207  
 FT /label=Transmembrane\_domain  
 FT 240..258  
 FT /label=Transmembrane\_domain

XX MO200142288-A2.  
 XX 14-JUN-2001.

XX 07-DEC-2000; 2000MO-US33382.  
 XX 10-DEC-1999; 9905-0172852.  
 XX 22-DEC-1999; 9905-0171732.  
 XX 14-JAN-2000; 2000US-0176148.  
 XX 21-JAN-2000; 2000US-0177331.

XX (INCY-) INCYTE GENOMICS INC.

XX Burford N, Baughn MR, Au-Young J, Yang J, Lu DAM, Reddy R;

XX WPI; 2001-381635/40.  
 XX N-PSDB; AAD08853.

XX New human G-protein coupled receptor polypeptides for diagnosing,  
 XX preventing, and treating cell proliferative, neurological,  
 XX cardiovascular, gastrointestinal, autoimmune and metabolic disorders -  
 XX Claim 1; Page 142; 175pp; English.

XX The present sequence is human G-protein coupled receptor-19 (GRC-19)  
 XX protein. GRC-19 is useful in somatic or germ-line gene therapy to correct  
 XX a genetic deficiency, to express a conditionally lethal gene product and  
 XX to express a protein which affords protection against intracellular  
 XX parasites and also for diagnosis of disorders associated with expression  
 XX of GRC-19. GRC-19 is also useful for generating hybridisation probes useful  
 XX in mapping the naturally occurring genomic sequences and to create  
 XX knock-in humanised animals (pigs) or transgenic animals (mice or rats) to  
 XX model human diseases. GRC-19 is used to diagnose, prevent and treat  
 XX proliferative disorders (actinic keratosis, arteriosclerosis, cirrhosis,  
 XX hepatitis and cancer); cancer (breast, bladder, bone marrow, brain,  
 XX uterus cancer, leukemia, adenocarcinoma, lymphoma, melanoma and myeloma)  
 XX neurological disorders (epilepsy, stroke, Alzheimer's, Huntington's,  
 XX Parkinson's disease, multiple sclerosis, dementia and other central  
 XX nervous system disorders); cardiovascular disorders (angina pectoris,  
 XX hypertension, atherosclerosis, congestive heart failure);  
 XX gastrointestinal disorders (dysphagia, peptic esophagitis, esophageal  
 XX spasm, gastritis, gastric carcinoma, anorexia, nausea, abdominal angina,

CC pyrosis, pancreatitis, Crohn's disease, diarrhoea); autoimmune/  
 CC inflammatory disorders (acquired immunodeficiency syndrome (AIDS),  
 CC Addison's disease, allergies, anaemia, asthma, diabetes mellitus, atopic  
 CC dermatitis, glomerulonephritis, Grave's disease, osteoarthritis, fungal,  
 CC psoriasis, rheumatoid arthritis, ulcerative colitis, bacterial, viral,  
 CC parasitic, protozoal and helminthic infections) and metabolic disorders  
 CC (obesity, osteoporosis, viral infections).

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 22; Length 353;

Best Local Similarity 99.7%; Pred. No. 3.1e-156;

Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 61 FHPPFYLLANLAADFPAGIAYVFLMFTGTPSVSKTLVNRWFLRQGLDSSLTASLTNTL 120  
 QY 1 MNECHYKHMDFEENRSTNDVDMGTGKLYIVCGVFCLTFEFSNLYIAVYINRK 60  
 DB 1 MNECHYKHMDFEENRSTNDVDMGTGKLYIVCGVFCLTFEFSNLYIAVYINRK 60  
 QY 61 FHPPFYLLANLAADFPAGIAYVFLMFTGTPSVSKTLVNRWFLRQGLDSSLTASLTNTL 120  
 DB 61 FHPPFYLLANLAADFPAGIAYVFLMFTGTPSVSKTLVNRWFLRQGLDSSLTASLTNTL 120  
 QY 121 LVIAVERHMSIMRRVNSNLTFRKVTLLILLYMAIAIFPKGAVPTLGNCLNISACSSLA 180  
 DB 121 LVIAVERHMSIMRRVNSNLTFRKVTLLILLYMAIAIFPKGAVPTLGNCLNISACSSLA 180  
 QY 181 PIYSRSLVFWTWSNLAFLIMVVYRIYVYVYRKTNVLSPTSGSISRRRPMKMT 240  
 DB 181 PIYSRSLVFWTWSNLAFLIMVVYRIYVYVYRKTNVLSPTSGSISRRRPMKMT 240  
 QY 241 VMTVLGAFVVCWTPGLVLPDLGLNCRCQGVQVHKRMFLLLALLNSVYVNIISYKDEDM 300  
 DB 241 VMTVLGAFVVCWTPGLVLPDLGLNCRCQGVQVHKRMFLLLALLNSVYVNIISYKDEDM 300  
 QY 301 YGTMKMKICFSDENPERPSPRIPSTVLSRSDSGQYIEDISIGGANCNKSTS 353  
 DB 301 YGTMKMKICFSDENPERPSPRIPSTVLSRSDSGQYIEDISIGGANCNKSTS 353

RESULT 6

ABG96440 standard; Protein: 353 AA.

ABG96440;

11-DEC-2002 (first entry)

Human ovarian cancer marker OV77.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;  
 KW central nervous system disorder; bacterial meningitis; viral meningitis;  
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
 KW brain herniation; inflammation; encephalitis; testicular disorder;  
 KW nontuberculous granulomatous orchitis; connective tissue disorder;  
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;  
 KW histological type; carcinogenic; ovarian cancer marker.

XX Homo sapiens.

XX MO200271928-A2.

XX 19-SEP-2002.

XX 14-MAR-2002; 2002MO-US07826.

XX 14-MAR-2001; 2001US-276025P.

XX 10-AUG-2001; 2001US-276026P.

XX 19-SEP-2001; 2001US-323580P.

XX 26-SEP-2001; 2001US-324967P.

XX 26-SEP-2001; 2001US-325102P.

XX 26-SEP-2001; 2001US-325149P.



QY 61 FHEPEYLLANLAADFFAGIAVFLMFNTGPKVSKITLVNRMFLROGLDSSLTASTLNL 120  
 CC |||||||  
 CC 61 FHEPEYLLANLAADFFAGIAVFLMFNTGPKVSKITLVNRMFLROGLDSSLTASTLNL 120  
 Db |||||||  
 QY 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVAIAIFMGAVPLGNCICNTSACSLSA 180  
 CC |||||||  
 CC 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVAIAIFMGAVPLGNCICNTSACSLSA 180  
 Db |||||||  
 QY 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240  
 CC |||||||  
 CC 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240  
 Db |||||||  
 QY 241 VMTVLGAFVVCWTPGLVLEPLDGLNCRCQCVQVHKRMFLALLNSVNPPIISYKDEDM 300  
 CC |||||||  
 CC 241 VMTVLGAFVVCWTPGLVLEPLDGLNCRCQCVQVHKRMFLALLNSVNPPIISYKDEDM 300  
 Db |||||||  
 QY 301 YGTMKKMICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353  
 CC |||||||  
 CC 301 YGTMKKMICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353  
 Db |||||||

## SOLT 8

ABR48221  
 ID ABR48221 standard; protein; 353 AA.

AC ABR48221;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX

DE Human bladder cancer associated protein sequence SEQ ID NO.162.

KM Human; bladder cancer; cytostatic; gene therapy; vaccine.

OS Homo sapiens.

PN WO2003003906-A2.

PD 16-JAN-2003.

PF 03-JUL-2002; 2002WO-US21338.

PR 03-JUL-2001; 2001US-302814P.

PR 08-NOV-2001; 2001US-343705P.

PR 13-NOV-2001; 2001US-350666P.

PR 12-APR-2002; 2002US-372246P.

PA (BOSB-) EOS BIOTECHNOLOGY INC.

DR MPI; 2003-201532/19.

DR N-PSDB; ACC51036.

PT Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody

PS Claim 10; Page 285-286; 307pp; English.

CC The present invention describes a method for detecting a bladder cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in

CC various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications.

SO Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;  
 Best Local Similarity 99.7%; Pred. No. 3, 1e-196;  
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYKHMDFYNSRNTDPTVDMGTGKVIYLCVGFCLTFPSNSLVIAVTKNR 60  
 Db |||||||  
 Db 1 MNECHYKHMDFYNSRNTDPTVDMGTGKVIYLCVGFCLTFPSNSLVIAVTKNR 60  
 QY 61 FHEPEYLLANLAADFFAGIAVFLMFNTGPKVSKITLVNRMFLROGLDSSLTASTLNL 120  
 Db |||||||  
 Db 61 FHEPEYLLANLAADFFAGIAVFLMFNTGPKVSKITLVNRMFLROGLDSSLTASTLNL 120  
 QY 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVAIAIFMGAVPLGNCICNTSACSLSA 180  
 Db |||||||  
 Db 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVAIAIFMGAVPLGNCICNTSACSLSA 180  
 QY 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240  
 Db |||||||  
 Db 181 PIYSRSYLVEWTVSNLMAFLIMVYVLRIVYVKRKTNLSPHTSGSISRRTPMKLMKT 240  
 QY 241 VMTVLGAFVVCWTPGLVLEPLDGLNCRCQCVQVHKRMFLALLNSVNPPIISYKDEDM 300  
 Db |||||||  
 Db 241 VMTVLGAFVVCWTPGLVLEPLDGLNCRCQCVQVHKRMFLALLNSVNPPIISYKDEDM 300  
 QY 301 YGTMKKMICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353  
 Db |||||||  
 Db 301 YGTMKKMICFSEQENPERRPSRIPSTVLSRSDGSOYIEDSISOGAVCNKSTS 353

## RESULT 9

ABP59287  
 ID ABP59287 standard; protein; 353 AA.

AC ABP59287;

DT 10-MAY-2003 (first entry)

DE Human Edg7 receptor.

KM Human; Edg; receptor.

OS Homo sapiens.

PN WO2003006503-A1.

PD 23-JAN-2003.

PF 10-JUL-2002; 2002WO-US22346.

PR 11-JUL-2001; 2001US-0904099.

PA (CERE-) CERTEK.

PI Shankar G, Munning JN, Spencer JV;

DR MPI; 2003-221718/21.

PT New chimeric Edg receptor, useful in high-throughput screening assays, comprises extracellular and transmembrane domains of a first Edg receptor, and a chimeric intracellular domain of a second Edg receptor

PS Disclosure; Page 20; 71pp; English.

CC The present invention relates to Edg receptors (ABP59277-ABP59290). The Edg receptors, are useful in a high-throughput screening assay to identify compounds that bind to or modulate the activity of the polypeptide, in calcium mobilisation assays, binding assays, detection of



CC CAMP formation, or in reporter gene techniques.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;

Best Local Similarity 99.7%; Pred. NO. 3.1e-196; Mismatches 352; Conservative 0; Indels 1; Gaps 0;

```

QY 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
QY 61 FHFPFYLLANLAADFFAGIAVYFLMNTGVSSTLYVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPFYLLANLAADFFAGIAVYFLMNTGVSSTLYVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFWTVSNLMFLMVVYVLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
DB 181 PIYSRSYLVFWTVSNLMFLMVVYVLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
QY 241 VMTVLGAFVVCWTPGLVYLLDGLNCRGCGVQHVHRWFLALLNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLDGLNCRGCGVQHVHRWFLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

```

RESULT 10  
ID ABUS6733 standard; Protein: 353 AA.

AC ABUS6733;

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polypeptide #326.

XX Lung cancer-associated polypeptide; cytostatic; emphysema;

KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX Interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX WO200286443-A2.

XX 31-OCT-2002.

XX 18-APR-2002; 2002WO-US12476.

XX 18-APR-2001; 2001US-284770P.

XX 10-MAY-2001; 2001US-290492P.

XX 09-NOV-2001; 2001US-339245P.

XX 13-NOV-2001; 2001US-350666P.

XX 29-NOV-2001; 2001US-334370P.

XX 12-APR-2002; 2002US-372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

XX WPI; 2003-093161/08.

XX DR N-PSDB; ABX76462.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient

for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased  
PS expression in lung cancer -

XX Claim 27; Page 440; 453pp; English.

CC The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung  
CC cancer-associated polynucleotides and polypeptides are used for  
CC identifying a compound that modulates a lung cancer-associated  
CC polypeptide, for inhibiting proliferation of a lung cancer-associated  
CC cell to treat lung cancer in a patient and for treating a mammal having  
CC lung cancer by administering a modulatory compound identified. The  
CC method are useful for treating lung cancer, such as small cell lung  
CC cancer, non-small cell lung cancer or other benign or precancerous  
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive  
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial  
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides  
CC and polypeptides are useful for diagnostic purposes and as targets for  
CC screening for therapeutic compounds that modulate lung cancer, such as  
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated  
CC polypeptides of the invention.

XX Sequence 353 AA;

Query Match 99.5%; Score 1838; DB 24; Length 353;

Best Local Similarity 99.7%; Pred. NO. 3.1e-196; Mismatches 352; Conservative 0; Indels 1; Gaps 0;

```

QY 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
DB 1 MNECHYDKHMDFFNRSNTDVTVDWGTGKLYIVLCVGTFFCLIFPFSNSLYIAAVIKNRK 60
QY 61 FHFPFYLLANLAADFFAGIAVYFLMNTGVSSTLYVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPFYLLANLAADFFAGIAVYFLMNTGVSSTLYVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMVHNSLTKRRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFWTVSNLMFLMVVYVLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
DB 181 PIYSRSYLVFWTVSNLMFLMVVYVLRIVYVKKRTNVLSPHTSGSISRRTPKLTKMT 240
QY 241 VMTVLGAFVVCWTPGLVYLLDGLNCRGCGVQHVHRWFLALLNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLDGLNCRGCGVQHVHRWFLALLNSVNPPIIYSYKDEDM 300
QY 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKMKICFSGOENPERPRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

```

RESULT 11  
ID ABP81689 standard; Protein: 353 AA.

AC ABP81689;

DT 04-MAR-2003 (first entry)

DE Human lysophosphatidic acid receptor Edg7 protein SEQ ID NO:553.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related disease; cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX Homo sapiens.  
 OS  
 PN MO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US50107.  
 XX  
 PR 19-DEC-2000; 2000US-257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burner GC, Roush CL, Brown JP;  
 XX  
 PS WPI: 2003-046718/04.  
 DR N-PSDB; ABZ42535.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases  
 XX  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (1) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.  
 XX  
 SO Sequence 353 AA;  
 QY Query Match 99.5%; Score 1838; DB 24; Length 353;  
 Db Best Local Similarity 99.7%; Pred. No. 3.1e-196;  
 Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNECHYKHMDFNRSNTDTVDWMTGKLYIVLCVGTFFCLFFFSNSLYIAVINKR 60  
 Db 1 MNECHYKHMDFNRSNTDTVDWMTGKLYIVLCVGTFFCLFFFSNSLYIAVINKR 60  
 QY 61 FHPEFYLLANLAADFFAGIAYVFLMNTGPKVSKLTVMRMLRQGLDSSLTASLTNL 120  
 Db 61 FHPEFYLLANLAADFFAGIAYVFLMNTGPKVSKLTVMRMLRQGLDSSLTASLTNL 120  
 QY 121 LVIAVERHMSIMRMRVSNLTKKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180  
 Db 121 LVIAVERHMSIMRMRVSNLTKKRVTLILLVMAIAIFMGAVPTLGNCLCNISACSSLA 180

QY 181 PIYRSILVETVTSNLAFLIMVYVYLRITYYVRKKNVLSPHITSGISRRRPTMKLMT 240  
 Db 181 PIYRSILVETVTSNLAFLIMVYVYLRITYYVRKKNVLSPHITSGISRRRPTMKLMT 240  
 QY 241 VMTVLGAFVVCWTFGLVVLPLDGLNCRCQGVQVHKRMFLALLANSVNPPIYSKEDM 300  
 Db 241 VMTVLGAFVVCWTFGLVVLPLDGLNCRCQGVQVHKRMFLALLANSVNPPIYSKEDM 300  
 QY 301 YGTMKKMICFSQENPERPSPRIPSTVLSRSDTGSQYIEDSISGAVCNKSTS 353  
 Db 301 YGTMKKMICFSQENPERPSPRIPSTVLSRSDTGSQYIEDSISGAVCNKSTS 353  
 RESULT 12  
 AAY24242  
 ID AAY24242 standard; Protein: 353 AA.  
 XX  
 AC AAY24242;  
 XX  
 DT 13-SEP-1999 (first entry)  
 XX  
 DE Human EDG-5 receptor clone pc3-hedg5#28 protein.  
 XX  
 KW EDG-5; HEDG-5; receptor homologue; asthma; rheumatoid arthritis;  
 KW adult respiratory distress syndrome; cardiac ischemia; septic shock;  
 KW acute pancreatitis; psoriasis; acute cyclosporine nephrotoxicity;  
 KW early diabetic glomerulopathy; lung damage.  
 XX  
 OS Homo sapiens.  
 OS  
 PN MO9933972-A1.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 24-DEC-1998; 98WO-CA01193.  
 XX  
 PR 24-DEC-1997; 97US-0997803.  
 XX  
 PA (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.  
 XX  
 PI Chun JYM, Gupta AK, Munroe DG, Vyas TB;  
 XX  
 DR WPI: 1999-419106/35.  
 DR N-PSDB; MAX86747.  
 XX  
 PS Nucleotide sequences encoding mammalian EDG-5 receptors  
 CC Claim 13; Fig 4C; 87pp; English.  
 CC The present sequence is a human EDG-5 (HEDG-5) receptor homologue.  
 CC EDG-5 sequences may be used to test for aberrant expression of HEDG-5  
 CC and can accelerate diagnosis and proper treatment of conditions such as  
 CC adult respiratory distress syndrome, asthma, rheumatoid arthritis,  
 CC cardiac ischemia, acute pancreatitis, septic shock, psoriasis, acute  
 CC cyclosporine nephrotoxicity and early diabetic glomerulopathy, as well  
 CC as lung damage following exposure to cigarette smoke, asbestos, or  
 CC silica. HEDG-5 specific antibodies, inhibitors and ligands may be used  
 CC to treat inflammation or diseases including, viral, bacterial or fungal  
 CC infections, allergic responses, mechanical injury associated with  
 CC trauma, hereditary diseases, lymphoma or carcinoma, or other conditions  
 CC which activate the genes of kidney, lung, heart, lymphoid or tissues of  
 CC the nervous system.  
 XX  
 SO Sequence 353 AA;  
 QY Query Match 99.2%; Score 1834; DB 20; Length 353;  
 Db Best Local Similarity 99.4%; Pred. No. 8.5e-196;  
 Matches 351; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MNECHYKHMDFNRSNTDTVDWMTGKLYIVLCVGTFFCLFFFSNSLYIAVINKR 60  
 Db 1 MNECHYKHMDFNRSNTDTVDWMTGKLYIVLCVGTFFCLFFFSNSLYIAVINKR 60

```

QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMRVHNSLTKRKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMRVHNSLTKRKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIYVVKRKTIVLSPHSGSISRRTTPMKLMKT 240
DB 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIYVVKRKTIVLSPHSGSISRRTTPMKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRGCGVQVHVRWFLLLALNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRGCGVQVHVRWFLLLALNSVNPPIIYSYKDEDM 300
QY 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYEDSISOGAVCNKSTS 353

```

## RESULT 13

ABP56225  
ID ABP56225 standard; Protein: 353 AA.

XX ABP56225;  
DT 28-MAR-2003 (first entry)

DE Human EDG7 receptor protein sequence.

KW Rat; EDG7 receptor; receptor; cytosolic; cancer.

OS Homo sapiens.

XX Key Location/qualifiers

```

FT MISC-difference 57 /note= "unclear in specification"
FT MISC-difference 103 /note= "unclear in specification"
FT MISC-difference 118 /note= "unclear in specification"
FT MISC-difference 207 /note= "unclear in specification"
FT MISC-difference 305 /note= "unclear in specification"
FT MISC-difference 316 /note= "unclear in specification"
FT MISC-difference 338 /note= "unclear in specification"

```

XX JP2002238578-A.

PD 27-AUG-2002.

PF 20-FEB-2001; 2001JP-0043004.

PR 20-FEB-2001; 2001JP-0043004.

PA (NNSH ) NIPPON SHINYAKU CO LTD.

DR WPI; 2003-049457/05.

XX Rat EDG7 receptor protein, useful for diagnosing and treating cancers

PS Example 2; Fig 1; 19pp; Japanese.

XX The present invention describes rat EDG7 receptor protein (I). Also  
CC described: (1) a polynucleotide (II) encoding (I); (2) an oligonucleotide  
CC which can hybridise with (II) under a stringent conditions; and  
CC (3) a recombinant vector containing (II). (I) has cytosolic activity.  
CC (I) can be used for diagnosing and treating cancers. The present sequence  
CC represents a human EDG7 receptor protein, which is given in comparison

CC with the rat EDG7 receptor protein in an example from the present  
CC invention.

XX Sequence 353 AA;

Query Match 96.0%; Score 1775; DB 24; Length 353;  
Best Local Similarity 96.9%; Pred. No. 3,3e-189;  
Matches 342; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

QY 1 MNECHYDHMDPEYRSNTDIPVDDMTGTRKLVYLCVGFCEFLFEFSNLSVAAVYKRRK 60
DB 1 MNECHYDHMDPEYRSNTDIPVDDMTGTRKLVYLCVGFCEFLFEFSNLSVAAVYKRRK 60
QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLRQGLDSSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGVPVSKTLTVNRWFLRQGLDSSLTASLTNL 120
QY 121 LVIAVERHMSIMRMRVHNSLTKRKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
DB 121 LVIAVERHMSIMRMRVHNSLTKRKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180
QY 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIYVVKRKTIVLSPHSGSISRRTTPMKLMKT 240
DB 181 PIYSRSYLVFMTVSNLMAFLIMVYVYLRIYVVKRKTIVLSPHSGSISRRTTPMKLMKT 240
QY 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRGCGVQVHVRWFLLLALNSVNPPIIYSYKDEDM 300
DB 241 VMTVLGAFVVCWTPGLVYLLPLDGLNCRGCGVQVHVRWFLLLALNSVNPPIIYSYKDEDM 300
QY 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYEDSISOGAVCNKSTS 353
DB 301 YGTMMKMICFSQENKERRPRSRIPSTVLSRSDTGSQYEDSISOGAVCNKSTS 353

```

## RESULT 14

ABBI2399  
ID AABI2399 standard; Protein: 354 AA.

XX AABI2399;

DT 13-NOV-2000 (first entry)

DE Human HOFNH30 protein.

KW HOFNH30; G-protein coupled receptor; 7TM receptor; vaccine;  
KW cancer; inflammation; autoimmune disease; Crohn's disease;  
KW allergy; asthma; rheumatoid arthritis; CMS inflammation;  
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;  
KW multiple sclerosis; stroke; osteoporosis; cardiovascular; kidney;  
KW liver; hypotension; hypertension; acquired immune deficiency syndrome;  
KW AIDS; male pattern baldness; bacterial; fungal; protozoan;  
KW viral infections.

XX Homo sapiens.

PN WO200035954-A1.

PD 22-JUN-2000.

PF 17-DEC-1999; 99WO-US30177.

PR 18-DEC-1998; 98US-0215072.

PR 04-JUN-1999; 99US-0325897.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PI Tsui P, Ellis CE, Sathe GM, Van Horn S, Ames RS, Foley JJ;

DR Fitzgerald LR, Sarau HM, Chambers JK;

DR WPI; 2000-431572/37.

PT N-PSDB: AAA63092.

XX New human G-protein coupled receptor, designated HOFNH30, useful for

treating infections, and disorders including cancers, diabetes, asthma, and Parkinson's disease.

Claim 2; Page 41-42; 44pp; English.

CC The present sequence is the novel human G-protein coupled receptor, HORNH30. The HORNH30 receptor may be expressed in human embryonic kidney 293 (HEK293) cells. This allows ligand binding assays to be carried out. The HORNH30 DNA and protein may be used for diagnosing or treating cancer, inflammation, autoimmune disease, Crohn's disease, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, stroke, osteoporosis, cardiovascular disease, kidney disease, liver disease, hypotension, hypertension, acquired immune deficiency syndrome (AIDS), male pattern baldness, and bacterial, fungal, protozoan and viral infections.

Sequence 354 AA;

Query Match 95.9%; Score 1772.5; DB 21; Length 354;  
Best Local Similarity 96.0%; Pred. No. 6.3e-189;

Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
QY 1 MNECHYKHMDFEYNSNTDVTDDMTGKLYIVLCVGTFFCLTFEFSNSLVIAAVINRK 60
DB 1 MNECHYKHMDFEYNSNTDVTDDMTGKLYIVLCVGTFFCLTFEFSNSLVIAAVINRK 60
QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGPVSKTLVNRWFLROGLDLSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGPVSKTLVNRWFLROGLDLSLTASLTNL 120
QY 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVMAIAFNGAVPTLGWNCICNISACSSLA 180
DB 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVMAIAFNGAVPTLGWNCICNISACSSLA 180
QY 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
DB 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIYSKDEDM 300
DB 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIYSKDEDM 300
QY 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 354
```

Result 15

56224

ABP56224 standard; Protein; 354 AA.

AC ABP56224;

DE 28-MAR-2003 (first entry)

DE Rat EDG7 receptor protein SEQ ID NO:1.

DE Rat; EDG7 receptor; receptor; cytosolic; cancer.

OS Rattus norvegicus.

PN JP2002238578-A.

PD 27-AUG-2002.

PF 20-FEB-2001; 2001JP-0043004.

PR 20-FEB-2001; 2001JP-0043004.

PA (NNSH) NIPPON SHINYAKU CO LTD.

DR WPI; 2003-049457/05.

DR N-PSDB; ABZ21907.

PT Rat EDG7 receptor protein, useful for diagnosing and treating cancers

PS Claim 1; Page 12; 19pp; Japanese.

CC The present sequence represents rat EDG7 receptor protein (I). Also described: (1) a polynucleotide (II) encoding (I); (2) an oligonucleotide which can hybridize with (II) under a stringent conditions; and (3) a recombinant vector containing (II). (II) has cytosolic activity. (I) can be used for diagnosing and treating cancers.

Sequence 354 AA;

Query Match 91.9%; Score 1697.5; DB 24; Length 354;

Best Local Similarity 91.0%; Pred. No. 1.5e-180;

Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

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QY 1 MNECHYKHMDFEYNSNTDVTDDMTGKLYIVLCVGTFFCLTFEFSNSLVIAAVINRK 60
DB 1 MNECHYKHMDFEYNSNTDVTDDMTGKLYIVLCVGTFFCLTFEFSNSLVIAAVINRK 60
QY 61 FHFPEYLLANLAADFFAGIAYVFLMNTGPVSKTLVNRWFLROGLDLSLTASLTNL 120
DB 61 FHFPEYLLANLAADFFAGIAYVFLMNTGPVSKTLVNRWFLROGLDLSLTASLTNL 120
QY 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVMAIAFNGAVPTLGWNCICNISACSSLA 180
DB 121 LVIAVERHMSIMRRVHNSLTKKRVTLILLVMAIAFNGAVPTLGWNCICNISACSSLA 180
QY 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
DB 181 PIYSRSYLIVFWTVSNLMAFLIMVYVRIYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIYSKDEDM 300
DB 241 VMTVLGAFVVCWPTGVLVLLPLDGLNCRCQGVQVHKRFFLLALLNSVYVNPPIYSKDEDM 300
QY 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKMICFSOE-NPERRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 354
```

Search completed: August 18, 2003, 15:09:49  
Job time : 85 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 15:04:54 ; Search time 42 Seconds  
(without alignments)  
808.275 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848  
Sequence: 1 MNECHYDKHMDFFYRNSNTD.....GSQYIEDSISGAVCNKSTS 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Cal number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES.

Result No.	Score	Query Match	Length	DB ID	Description
1	948.5	51.3	364	2	JC5293 lysophosphatidic a
2	541	29.3	383	2	Edg-1 orphan recep
3	540.5	29.2	362	2	sphingosine 1-phos
4	537	29.1	378	2	JC5245 G protein-coupled
5	533.5	28.9	381	2	A35300 G protein-coupled
6	499	27.0	352	2	JC1465 probable G protein
7	352	19.0	330	2	A55689 G protein-coupled
8	351	19.0	330	2	SA0454 G protein-coupled
9	347	18.8	473	2	A33117 cannabinoid recept
10	341	18.5	472	2	SI1595 cannabinoid recept
11	327.5	17.7	362	2	I65990 G protein-coupled
12	326.5	17.7	363	2	S48697 probable G protein
13	326	17.6	325	2	JC5592 melanocortin-5 rec
14	325	17.6	372	2	I49008 melanocortin-5 rec
15	314	17.0	325	2	I46416 melanocyte stimula
16	312	16.9	325	2	JC2193 melanocortin recep
17	310.5	16.8	332	2	AS7055 melanocortin recep
18	306	16.6	325	2	JN0764 melanocortin recep
19	302.5	16.4	180	2	E48909 G protein-coupled
20	295	16.0	323	2	SA3850 melanocortin 3 rec
21	294	15.9	390	2	JN0268 serotonin receptor
22	293	15.9	389	2	S68422 serotonin receptor
23	292	15.8	390	2	SS8126 serotonin receptor
24	291	15.7	323	2	S36636 melanocortin recep
25	290.5	15.7	386	2	A42688 serotonin receptor
26	289.5	15.7	386	2	SS4153 serotonin receptor
27	289.5	15.7	386	2	SI8637 serotonin receptor
28	289	15.6	347	2	S70364 cannabinoid recept
29	287.5	15.6	360	2	B46647 melanocortin recep

30	283	15.3	374	2	I77467 serotonin receptor
31	279.5	15.1	377	2	S68423 serotonin receptor
32	273.5	14.8	377	2	B30341 G protein-coupled
33	272	14.7	360	2	S36750 cannabinoid recept
34	272	14.7	377	2	A53279 serotonin receptor
35	270	14.6	515	2	A40491 serotonin receptor
36	267	14.4	501	2	JH0447 alpha-1A-adrenergic
37	267	14.4	572	2	I39369 alpha-1A-adrenergic
38	265	14.3	509	2	A47174 serotonin receptor
39	264	14.3	332	2	JC1229 adenosine receptor
40	261	14.1	517	2	A45121 alpha-1B adrenergic
41	260	14.1	314	2	S71420 melanocortin 1 rec
42	258	14.0	477	2	S71323 alpha-1A adrenergic
43	258	14.0	515	2	JC1525 alpha-1A adrenergic
44	257.5	13.9	560	2	A38731 alpha-1A adrenergic
45	256.5	13.9	366	2	S26048 serotonin receptor

## ALIGNMENTS

## RESULT 1

JC5293 lysophosphatidic acid receptor - human

N:Alternate names: Edg2 protein

C:Species: Homo sapiens (man)

C>Date: 16-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 10-Dec-1999

C:Accession: JC5293

R:An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.

Biochem. Biophys. Res. Commun. 231, 619-622, 1997

A:Title: Molecular cloning of the human Edg2 protein and its identification as a func

A:Reference number: JC5293; MUID:9724397; PMID:9070858

A:Contents: lung

A:Accession: JC5293

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-364 <ANA>

A:Cross-references: GB:U08011; NID:91857424; PIDN:AMC51139.1; PID:91857425

C:Superfamily: G protein-coupled receptor edg-1

Query Match	51.3%	Score 948.5	DB 2	Length 364
Best Local Similarity	51.6%	Pred. No. 2.9e-74		
Matches 175	Conservative 76	Mismatches 75	Indels 13	Gaps 5
QY	1	MNE--CHYDKHMDFFYRNSNTDVTDDW--TGFTLVIVLCVGFPECLFFFSNSLYIAAYIK 57		
DB	19	MMEEPPFYLLANLAADDFAGIAYVFLMFTGVSRTLVNRFLLROGLDSSLTASTL 117		
QY	58	NKKFHPFYLLANLAADDFAGIAYVFLMFTGVSRTLVNRFLLROGLDSSLTASTL 117		
DB	77	NRRFHPFYLLANLAADDFAGIAYVFLMFTGVSRTLVNRFLLROGLDSSLTASTL 136		
QY	118	TNLVIAVERHMSIRMRVHNSMLTKRYTLTLILVMAIAIENGAVPTLGMCNLSACS 177		
DB	137	ANLAIATIERHITVFRMOLHFRMSNRVVVIVVIMVAIYGAIPSGVANCICDIENS 196		
QY	178	SLAPYSYLYEVNVMFLINVVYLRVYVKKRNTVLSHTSGSISRRTPKTL 237		
DB	197	NNAPLSDSYLVFMAELVTFVNVVLAHFGVROKRTMRSRSHSGPRRRRTPMASL 256		
QY	238	MKTVMTVLGAFAVVCWTPGLVVLPLDLGNCROGVQVHRVFWFLALLALNSVVPPIITYSKD 297		
DB	257	LKTVVIVVGAFLICWTPGLVVLPLDLGNCROGVQVHRVFWFLALLALNSVVPPIITYSKD 315		
QY	298	EDMTGTRKMKICFSQENP-----ERRPSRIPSTVYS 329		
DB	316	KEMSATFFROIICCORSENPPTGPTSSDRSASLMTHTILA 354		

## RESULT 2

Edg-1 orphan receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 24-Sep-1999  
 C/Accession: J53870  
 R/Lao, D.C.; Browe, C.S.; Gaskin, A.A.; Borden, J.M.; MacLennan, A.J.  
 Gene 149, 331-336, 1994  
 A/Title: Cloning of the rat edg-1 immediate-early gene: expression pattern suggests dive  
 A/Reference number: J53870; MUID:95047498; PMID:7959012  
 A/Accession: J53870  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-383 <RES>  
 A/Cross-references: EMBL:U10303; NID:9595396; PIDN:AAA83418.1; PID:9595397  
 C/Superfamily: G protein-coupled receptor edg-1

Query Match 29.3%; Score 541; DB 2; Length 383;  
 Best Local Similarity 34.2%; Pred. No. 4.3e-39;  
 Matches 117; Conservative 77; Mismatches 128; Indels 20; Gaps 7;

27 GTKIVLCVGFECLEFFNSLVIAVINKRKHFFHYLLANLAADFAGIAYFL 86  
 45 GIKLTAVFEL-LICCLILENIFVLTIMTKKFFHMYFIGNLALSDLAGAVIYAN 102  
 87 MENTGPVSKITLVNRKRLGGLDSSLTASLTNLLVAVRHSIMRVRHSNLTTRKRYT 146  
 103 LLSGATTYKLTLPQWELREGSMFVALSAYSLATAIERYITMLKMLHNGSNSSRF 162  
 147 LLLILVAIAIFMGAVPTLGNCLNISACSLAPIYSRSLVFWYSNLMALFLMVY 206  
 163 LLISACWVISTLGLPLMGNCISLSSCSTVPLVHKHILCTVYFTLLISTVLY 222  
 207 LRIYVYKRTNVSPTSGSISRRT--PMKLMTWVTVGAIVCWTPLVAVLPD-G 263  
 223 CRISLVTRRRLTFKRNKISKASRSEKSLALKYIVIVSVIACAPFIILLDVG 282  
 264 LNCQGVQVHKRFFLLALINSVNPITISYKDEDMYTKMKICFSQENPE----R 318  
 283 CKATCKTILYKAEFVLAVINSCTNPIYTLFKNKRAFRIRIISCKCPNGDSAGKFK 342  
 319 RPSRIPSVLSR--SDGSOYIEDS-----ISGAVCNKS 351  
 343 RPT-IPGMEFSRKSNDNSHPQKDDGNDPMTIMSSGNVSS 383

RESULT 3  
 JC7559  
 sphingosine 1-phosphate receptor - zebra fish  
 N/Alternate names: endothelial differentiation gene 1 receptor  
 C/Species: Brachydanio rerio (zebra fish)  
 C/Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 03-Aug-2001  
 C/Accession: JC7559  
 A/Map position: 10m, D.S.; Ungar, A.R.; Lynch, K.R.  
 A/Chem. Biochem. Res. Commun. 279, 139-143, 2000  
 A/Title: Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate receptor  
 A/Reference number: JC7559; MUID: 20363813; PMID:11112429  
 A/Accession: JC7559  
 A/Molecule type: DNA  
 A/Residues: 1-362 <IMA>  
 A/Cross-references: GB:AF321294  
 C/Comment: This receptor, a G protein-coupled receptor, mediates sphingosine 1-phosphate  
 C/also functions in the developing central nervous system in cell proliferation, apopto  
 C/Genetics:  
 A/Gene: edg1  
 C/Superfamily: G protein-coupled receptor edg-1  
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.2%; Score 540.5; DB 2; Length 362;  
 Best Local Similarity 34.3%; Pred. No. 4.5e-39;  
 Matches 113; Conservative 68; Mismatches 129; Indels 19; Gaps 5;  
 41 CLTFFNSLVIAVINKRKHFFHYLLANLAADFAGIAYFLMNTGPVSKITLVN 100  
 35 CCEITLNVAVLTIMTKKFFHMYFIGNLALSDLAGAVVYANILSGANTYKLTPT 94  
 101 RMLPRLGGLDSSLTASLTNLLVAVRHSIMRVRHSNLTTRKRVTLILLVAIAIFMG 160

DB 95 QMFREGSMFVALASVSLAIAIERHLIMLKRLHNGKTCVEMLISTVWPIAAILG 154  
 161 AVPTLGNCLNISACSLAPIYSRSLVFWYSNLMALFLMVYLRITVYRKTNVL 220  
 155 GLPVMGNKIDISNCGSVPLVHKAYILFCTVFSVILMAIVLVARIVALTFRSKL 214  
 221 ----SPTSGSISRRTPMKIMKTVMVGLAFVVCWPGVLPLDGLNCR--OCGVQHV 274  
 215 VERRVANGRGSKNSSEKSMALLKTVIIVLSCFIACMAPLFIILLD--VACQTFCSILYK 273  
 275 KRMFLALINSVNPITISYKDEDMYTKMKICFSQENPE---RPSRIPSVLSRS 331  
 274 AEMFLALAVLSAMPPLITVLTSMERRAFITKMLNCGVQVPSGKFSRPIMGAEFTSKS 333  
 332 DTGSOYIEDS-----ISGAVCNKS 351  
 334 DNSHPMKNDPEYSRPRETVSSGNITSS 362

RESULT 4  
 JC5245  
 G protein-coupled receptor - human  
 C/Species: Homo sapiens (man)  
 C/Date: 13-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C/Accession: JC5245  
 R/Yanaguchi, F.; Tokuda, M.; Hatake, O.; Brenner, S.  
 Biochem. Biophys. Res. Commun. 227, 608-614, 1996  
 A/Title: Molecular cloning of the novel human G protein-coupled receptor (GPCR) gene  
 A/Reference number: JC5245; MUID:97032811; PMID:8878560  
 A/Accession: JC5245  
 A/Molecule type: DNA  
 A/Residues: 1-378 <IYM>  
 A/Cross-references: EMBL:X83864; NID:91770395; PIDN:CAA58744.1; PID:91770396  
 C/Comment: This protein transduces hormone and neurotransmitter signals into intracel  
 C/Genetics:  
 A/Gene: edg-3  
 A/Map position: 9q22.1-q22.2  
 C/Superfamily: G protein-coupled receptor edg-1  
 C/Keywords: G protein-coupled receptor

Query Match 29.1%; Score 537; DB 2; Length 378;  
 Best Local Similarity 34.9%; Pred. No. 9.5e-39;  
 Matches 122; Conservative 68; Mismatches 124; Indels 36; Gaps 9;

27 GTKIVLCVGFECLEFFNSLVIAVINKRKHFFHYLLANLAADFAGIAYFL 86  
 38 GSTLTIVLFL--VICSPVLENIMVLAIMRNKFFHMYFIGNLALCDLAGIAYKN 95  
 87 MENTGPVSKITLVNRKRLGGLDSSLTASLTNLLVAVRHSIMRVRHSNLTTRKRYT 146  
 96 LMSGKTFSSPTVWFLREGSMFVALGASTCSLATAIERHLIMTKRPPDANKRRHV 155  
 147 LLLILVAIAIFMGAVPTLGNCLNISACSLAPIYSRSLVFWYSNLMALFLMV 205  
 156 LLIMCMVLAFVTLGALPLIGNCLNHPDCSTILPLSKYIAF-CISIFALIVTVIL 214  
 206 YLRITVYKRTNVSPTSGSISRRTPMKIMKTVMVGLAFVVCWPGVLPLDGLN 265  
 215 YARIVYKSSSRKVAHNNSERS----MALFTVIVVSVFIACMSPLFIILFDIVA 268  
 266 CR--QCGVQVHKRFFLLALINSVNPITISYKDEDMYTKMKICF-----SQE 314  
 269 CRVQACPLIFKRAQFVLAVLSAMNPVITVTLASKEMRAFFRLVCALVGRGARASPT 328  
 315 NPERRPRIPTSVLSRSDTGSQYED-----STISGAVCN 349  
 329 QPALDPSRKSNSNSHSPRYKEDLPHDPSCINDKNAALQNGIFCN 378

RESULT 5  
 A35300  
 G protein-coupled receptor edg-1 - human

C:Species: Homo sapiens (man)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 24-Sep-1999  
C:Accession: A35300  
R:HLA, T.: Mactag T.  
J. Biol. Chem. 265, 9308-9313, 1990  
A:Title: An abundant transcript induced in differentiating human endothelial cells encod  
A:Reference number: A35300; MUID:90264425; PMID:2160972  
A:Accession: A35300  
A:Molecule type: mRNA  
A:Residues: 1-381 <HLA>  
A:Cross-references: GB:M31210; NID:g181948; PIDN:AAA52336.1; PID:g181949  
C:Genetics:  
A:Gene: GDB:ECGF1  
A:Cross-references: GDB:127754; OMIM:131222  
A:Map position: 22q13-22q13  
A:Superfamily: G protein-coupled receptor edg-1  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match	28.9%;	Score 533.5;	DB 2	Length 381;
Best Local Similarity	31.7%;	Pred. No. 1.9e-38;		
Matches 114;	Conservative 78;	Mismatches 131;	Indels 37;	Gaps 7

QY 5 HYDKHMEFFYRSTDEVDMDTGTRKLYVLGCVGEFFCLFEFFSNLSLAAYAKRNKFRHP 64  
Db HYN-----YGKLNISADKRENSIKLNSVFI--LICCFILLENFVLITMKTKKFRHP 79  
QY 65 FYLLANLAAADFAAGIAYFYFMERTGVSCTLYVNRWFYLAQGLDSSLTASLNLVLYA 124  
Db MYEYIGLNALSDLLAGVAYTANLLLSGATYTKPIPAQWFLREBGSFYVALSASFSLAIA 139  
QY 125 VERHSMIRMRVHNSLTKRKRYTLTLLMAWAIAIFGAPPTLGMNCLISACSSAPLAYS 184  
Db IERYITLKMKLHNGSNNEFLLELISACWVSLILGPIPMGNCLISLSCSSTVPLIYH 199  
QY 185 RSYLYEVTVSLLMAFLIMVYVYLTPYYVYKREKTNLSPHIS--GTSRRRTPKMLKTYMT 243  
Db KHTLLECTYVTLTLLSLTLYICRYSLWPRRSRLYPRKNTSKASRSSENAVLATYII 259  
QY 244 VLGAFFVVCWPTGLVYLPID--GLNCRQCQGVQHYKRWFLTLLALNSVYNPLYSYKDEDM-Y 301  
Db VLASFIAICWAPLELITLLLDVGCQKVCOTDLTFRAEFYVLAVLNSGTNPILYITLTKEMR 319  
QY 302 GTMKMKIC-----FSQ-----ENPRRRSRRLPSVLSNDPS 335  
Db AFIIRMSCCKPSPGDSAGKFRKRPITAGMEFSKSKSDNSSHPKDEGNDPETMTSGGNVS 379

**RESULT 6**

C:Observable G protein-coupled receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jul-2000  
 C:Accession: J01465  
 R:Okazaki, H.; Ishizaka, N.; Sakurai, T.; Kurokawa, K.; Goto, K.; Kumada, M.; Takuwa, Y.  
 Biochem. Biophys. Res. Commun. 190, 1104-1109, 1993  
 A:Title: Molecular cloning of a novel putative G protein-coupled receptor expressed in the  
 A:Reference number: J01465; MUID:93176155; PMID:8382486  
 A:Accession: J01465  
 A:Molecule type: mRNA  
 A:Residues: 1-352 <OKA>  
 A:Cross-references: GB:AB016931; NID:g3445557; PIDN:BAA32454.1; PID:g3445558  
 A:Experimental source: aortic smooth muscle  
 C:Superfamily: G protein-coupled receptor edg-1  
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F:35-59/Domain: transmembrane #status predicted <TM1>  
 F:67-95/Domain: transmembrane #status predicted <TM2>  
 F:110-128/Domain: transmembrane #status predicted <TM3>  
 F:148-173/Domain: transmembrane #status predicted <TM4>  
 F:190-210/Domain: transmembrane #status predicted <TM5>  
 F:234-255/Domain: transmembrane #status predicted <TM6>  
 F:272-293/Domain: transmembrane #status predicted <TM7>  
 F:179/Binding site: carbonyl(ate) (asn) (covalent) #status predicted  
 F:114/145, 218, 219, 329, 330, 331, 332/Binding site: phosphate (Ser) (covalent) #status predicted  
 F:114/145, 218, 219, 329, 330, 331, 332/Binding site: phosphate (Ser) (covalent) #status predicted

F:313/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	27.0%	Score 499;	DB 2;	Length 352;
Best Local Similarity	33.2%	Pred. No. 1.7e-35;		
Matches 113;	Conservative 69;	Mismatches 118;	Indels 40;	Gaps 9

[illegible]

## RESULT

G protein-coupled receptor 3 - human  
 N:Alternate names: G protein-coupled receptor GPR3; orphan G-protein-coupled receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Mar-1995 #sequence,revision 03-Mar-1995 #text,change 19-May-2000  
 C:Accession: A55689; S58521, C55733  
 R:Litman, T.P.; Klefer, J.; Liu, M.L.; Baker, E.; Sutherland, G.R.; Shine, J.  
 Genomics 24, 391-394, 1994  
 A:Title: Isolation and chromosomal localization of a novel human G-protein-coupled re  
 A:Reference number: A55689; MUID:95213036; PMID:7698767  
 A:Accession: A55689  
 A:Status: preliminary  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-330 <ITS>  
 A:Cross-references: GB:IJ2830; GB:IJ2831; NID:g602311; PIDN:AAAT3560.1; PID:g602312  
 R:Engelstern, D.; Denen, J.F.; Labbe, O.; Hayashi, Y.; Refetoff, G.; Parm  
 Biochem. J. 309, 837-843, 1995  
 A:Title: Molecular cloning of an orphan G-protein-coupled receptor that constitutivel  
 A:Reference number: S58521; MUID:95366960; PMID:7659700  
 A:Accession: S58521  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-330 <EGG>  
 A:Cross-references: GB:X83956; NID:g1061125; PIDN:CAAB8787.1; PID:g1061126  
 R:Marchase, A.; Doeherty, J.M.; Nguyen, T.; Helber, M.; Cheng, R.; Heng, H.H.O.; Tsu  
 Genomics 23, 609-618, 1994  
 A:Title: Cloning of human genes encoding novel G protein-coupled receptors.  
 A:Reference number: A55733; MUID:95154831; PMID:7851889  
 A:Accession: C55733  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-292 <MAR>  
 A:Cross-references: GB:U13668; NID:g577416; PIDN:AAA64594.1; PID:g577417  
 C:Genetics:  
 A:Gene: GDB:GPR3  
 A:Cross-references: GDB:371695; OMIM:600241  
 A:Map position: 1p36.1-p34.3  
 C:Superfamily: melanocortin receptor  
 C:Keywords: G protein-coupled receptor; transmembrane protein



Best Local Similarity 30.08; Pred. No. 7.5e-23;  
Matches 96; Conservative 58; Mismatches 116; Indels 42; Gaps 11;

QY 32 IVLCV-GTFECLFFFSNSLVIAVINKRKHFEFFYLLANLAADFFAGIAYF---LM 87  
D 45 VVLCISG---LVSCENALVVALIVGPAFRAMPFLVGLAVADLAGLGLVHFAAV 100  
QY 88 FNTGPAVKRTLVNRMFLRQGLDSSLASLTNLVIAVERMSIMR-MRVHSNLTKKRYT 146  
D 101 FCTISAEKSLVL-----VGLAAMAFASIGSLATVDRSLSYNMLTYSETVTRTY 154  
QY 147 LLLVLAIAIFMGAVPLIGWNCNCSACSLAPIYSRSVLPVWVSNLMALIMVYV 206  
D 155 VMLAVVGGALGLLPLVLANNCIDGLTTCGVPL-SKNLVLVLAIAFFVFGIMQLY 213  
QY 207 LRIIVYVKKRTNVLSPHTSGISRRRP-----MLMKVTMTVLGAFFVCGTPEGVL 259  
D 214 AQICRIYCRHAQQL-----ALQRLHPASHYVATRKGIATLAVVAGFACWMLPFVYC 267  
QY 260 PLDGLNRCQGVQVYKRMFLIAL---NSVVPITISYDEDMGTMKMKICFSGEN 315  
D 268 LL-----GDASPLLYTLLPATYNSMINPIYAFRNOVDOKVLAVCCSSSK 319  
QY 316 PERPSRIPSTV 327  
D 320 IPRR-SRSPDY 330

# RESULT 8

G protein-coupled receptor GPCR21 - mouse  
S40454

C:Species: Mus musculus (house mouse)  
C:Date: 19-May-1994 #sequence, revision 10-Nov-1995 #text, change 20-Jun-2000  
C:Accession: S40454  
R:Seiki, Y.; Ueno, S.; Mizuno, R.; Nishimura, T.; Fujimura, H.; Nagai, Y.; Yanagihara, T.  
A:Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which  
FEBS Lett. 336, 317-322, 1993  
A:Reference number: S40454; MUID:94085630; PMID:8262253  
A:Accession: S40454  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-330 <SAE>  
A:Cross-references: GB:D21062; NID:g455487; PIDN:BA04641.1; PID:g455488  
C:Superfamily: melanocortin receptor  
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

## Query Match

19.08; Score 351; DB 2; Length 330;

Best Local Similarity 30.08; Pred. No. 9.2e-23;  
Matches 101; Conservative 61; Mismatches 125; Indels 50; Gaps 12;

QY 15 NRSTVDVDMTGKLV-----IVLCV-GTFECLFFFSNSLVIAVINKRKHFE 65  
D 20 NVSSVDVEEPTGPTLLPSRAWDVVLISGT-----LVSCENALVVALIVGPAFRAPM 75  
QY 66 YLLANLAADFFAGIAYFVL---FNTGPAVKRTLVNRMFLRQGLDSSLTASTNLV 122  
D 76 FLVGSIAVDLGLGLVHFAADFCISGPEML-----MLVGLAMAFATASIGSLA 129  
QY 123 IAVERNHSIMR-MRVHSNLTKKRYTLLVLAIAIFMGAVPLIGWNCNCSACSLAP 181  
D 130 ITVDRIYSLVNALIYSETVTRTYVMAVLAIVGALDGLVPLVLANNCROGLTTCGVYR 189  
QY 182 IYSRSIYFVTSNLMALIMVYVLRIVYVKKRTNVLSPHTSGISRRRP----- 234  
D 190 L-SKNHVLVLAIAFFVFGIMQLYAOICRIYCRHAQQL-----ALQRLHPASHVAT 242  
QY 235 MKLMKVTMTVLGAFFVCGTPEGVLPLDGLNRCQGVQVYKRMFLIAL---NSVVP 290  
D 243 RKGIATLAVVAGFACWMLPFVYICL-----GDASPLRYTLLPATYNSMINP 294  
QY 291 IISYKDEDMGTMKMKICFSGENPERPSRIPSTV 327  
D 295 VIYAFRNOVDOKVLAIVCCSSSKIPRR-SRSPDY 330

## RESULT 9

A33117

cannabinoid receptor CB1 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jan-1993 #sequence, revision 22-Jan-1993 #text, change 05-Nov-1999

C:Accession: A33117; C55879

R:Matsumoto, L.A.; Lolait, S.J.; Brownstein, M.J.; Young, A.C.; Bonner, T.I.

Nature 346, 561-564, 1990

A:Title: Structure of a cannabinoid receptor and functional expression of the cloned

A:Reference number: A33117; MUID:90332039; PMID:2165569

A:Accession: A33117

A:Molecule type: mRNA

A:Residues: 1-473 <MAT>

A:Cross-references: GB:X55812; NID:g1552375; PIDN:CA039332.1; PID:g57249

R:Shire, D.; Carillon, C.; Kaghad, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.;

J. Biol. Chem. 270, 3726-3731, 1995

A:Title: An amino-terminal variant of the central cannabinoid receptor resulting from

A:Reference number: A55879; MUID:95181323; PMID:7876112

A:Accession: C55879

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-107 <SHI>

C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

## Query Match

18.88; Score 347; DB 2; Length 473;

Best Local Similarity 26.98; Pred. No. 3e-22;

Matches 80; Conservative 69; Mismatches 122; Indels 26; Gaps 6;

QY 31 VIIVCVGTFECLFFFSNSLVIAVINKRKHFE-PFYLLANLAADFFAGIAYFIMFN 89  
D 122 VLSLTGTFTFYL---ENLVLCVILHSRSLRCHPSHFGLSLAVADLSSVIFVSEVD 177  
QY 90 TGPVSKRTLVNRMFLRQGLDSSLTASTNLVIAVERMSIMR-VHSNL-TKKRYTL 148  
D 178 FHYHRKDSRNVFLFKIGVYASTAVSGSLFLAIDRIYSIHPLAKRYVPRKAVVA 237  
QY 149 ILLVMAIAIFMGAVPLIGWNCNCSACSLAPIYSRSYLVFWTSNLMALIMVYVLR 208  
D 238 FCLMKTAIVYAVPLIGWNCNCKLQVSCSDIFPLIDETVLEMT--GVTSVLLLFYIYAV 295  
QY 209 IYVYV-----KRTNVLSPHTSGT-----SRRTPMKMTKTYVTVLGAFFV 250  
D 296 MYLWKASHAVRNIGRTGKSLIHSDEGKVQVTRPDARMDIRLAKTLVLLVLI 355  
QY 251 CWTPEGLVPLDGLNRCQGVQVYKRMFLIALINSVYVPIYSYKDEDMGTMKKM 307  
D 356 CWGFLAIAIMYDVGVGNKKLKYFAICSMICLINSVNPITVYLRSKDLRHAFRSM 412

## RESULT 10

S17595

cannabinoid receptor CB1 - human

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence, revision 03-Feb-1994 #text, change 21-Jul-2000

C:Accession: S17595; S13668; A55879

R:Gerard, C.M.; Mollereau, C.; Vassart, G.; Parmentier, M.

Biochem. J. 279, 129-134, 1991

A:Title: Molecular cloning of a human cannabinoid receptor which is also expressed in

A:Reference number: S17595; MUID:92028798; PMID:1718258

A:Accession: S17595

A:Molecule type: mRNA

A:Residues: 1-472 <GER1>

A:Cross-references: EMBL:X54937; NID:g29914; PIDN:CA038699.1; PID:g29915

R:Gerard, C.; Mollereau, C.; Vassart, G.; Parmentier, M.

Nucleic Acids Res. 18, 7142, 1990

A:Reference number: S13668; MUID:91088303; PMID:2263478

A:Accession: S13668

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-472 <GER2>









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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 15:03:54 ; Search time 99 Seconds

(without alignments)  
920.127 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848  
Sequence: 1 MNECHYDKHMDFFYNRSNTD.....GSOYIEDSISGAVCNKSTS 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1772.5	95.9	354	4	Q9NRB8
2	929	50.3	194	11	Q8VDA1
3	899	48.6	296	11	Q8VDA2
4	716.5	38.8	251	13	Q8VDA4
5	598	32.4	123	6	Q95L85
6	548	29.7	382	11	Q9R235
7	546	29.5	382	11	Q9DC35
8	544.5	29.5	326	11	Q9NR35
9	543.5	29.4	378	11	Q9Z009
10	541.5	29.3	378	11	Q8BP20
11	540.5	29.2	362	13	Q9DDK4
12	539.5	29.2	326	11	Q9NR1
13	538	29.1	326	11	Q9NR4
14	537.5	29.1	326	11	Q9NR8
15	536	29.0	326	6	Q9BF5
16	534	28.9	326	6	Q9BF48

17	533.5	28.9	326	6	Q9BF49	Q9BF49 targetelaphus
18	533.5	28.9	326	6	Q9BF47	Q9BF47 okapia john
19	532	28.8	382	4	Q9NR48	Q9NR48 homo sapien
20	531.5	28.8	326	6	Q9BF63	Q9BF63 ochotona hy
21	531.5	28.8	326	11	Q9NR3	Q9NR3 erethizon d
22	531	28.7	326	11	Q9NR0	Q9NR0 cavia tscu
23	530.5	28.7	326	11	Q9NR7	Q9NR7 agouti tacz
24	530	28.7	326	11	Q9NR9	Q9NR9 hydrochoeru
25	530	28.7	384	13	Q9PU08	Q9PU08 fugu rubrip
26	529	28.6	326	6	Q9BF52	Q9BF52 megaptera n
27	529	28.6	326	11	Q9NR7	Q9NR7 muscardinus
28	528.5	28.6	326	11	Q9NR8	Q9NR8 castor cana
29	528	28.6	326	6	Q9BF70	Q9BF70 trichechus
30	528	28.6	326	6	Q9BF70	Q9BF70 amblysomus
31	528	28.6	326	6	Q9BF67	Q9BF67 macroscellid
32	528	28.6	326	6	Q9BF66	Q9BF66 elephantulu
33	527.5	28.5	326	6	Q9BF50	Q9BF50 hippopotamu
34	526.5	28.5	326	6	Q9BF87	Q9BF87 tadaria dr
35	525	28.4	326	6	Q9BF45	Q9BF45 ceratotheri
36	524.5	28.4	326	6	Q9BF76	Q9BF76 tamandua te
37	523.5	28.3	326	6	Q9BF46	Q9BF46 equus cabal
38	523.5	28.3	326	6	Q9BF57	Q9BF57 hylobates c
39	523.5	28.3	326	6	Q9BF72	Q9BF72 soxex arane
40	523	28.3	326	6	Q9BF69	Q9BF69 procavia ca
41	522	28.2	326	11	Q9NR9	Q9NR9 tamias stri
42	521	28.2	326	6	Q9BF75	Q9BF75 myrmecophag
43	521	28.2	326	6	Q9BF73	Q9BF73 condylura c
44	520.5	28.2	326	6	Q9BF44	Q9BF44 tapirus ind
45	520	28.1	326	6	Q9BF60	Q9BF60 lemur calta

## ALIGNMENTS

## RESULT 1

ID	Q9NRB8	PRELIMINARY:	PRT:	354 AA.
AC	Q9NRB8;			
DT	01-OCT-2000 (TRENBLREL. 15, Created)			
DI	01-OCT-2000 (TRENBLREL. 15, Last sequence update)			
DT	01-MAR-2003 (TRENBLREL. 23, Last annotation update)			
DE	G-protein coupled receptor EDG-7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20351181; PubMed=10891327;			
RA	Fitzgerald L.R., Dytko G.M., Sarau H.M., Mannan I.J., Ellis C.,			
RA	Lane P., Tan K.B., Wilton S., Bergsma D.J., Ames R.S., Foley J.J.,			
RA	Cambell D., McMillan L., Evans N., Elshourbagy N., Tsui P.,			
RT	"Identification of an EDG7 Variant, HOFN30, a G-Protein-Coupled			
RT	Receptor for Lysophosphatidic Acid."			
RL	Biochem. Biophys. Res. Commun. 273:805-810(2000).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL: AF236117; AAF91291.1; -			
DR	InterPro: IPR005385; EDG7_receptor.			
DR	InterPro: IPR00276; GPCR_Rhodopsin.			
DR	InterPro: IPR004065; LPAR_receptor.			
DR	Pfam: PF00001; 7tm_1; 1.			
DR	PRINTS: PR01560; EDG7RECEPTOR.			
DR	PRINTS: PR00237; GPCR_RHODOPSIN.			
DR	PRINTS: PR01527; LPARRECEPTOR.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Receptor; Transmembrane.			
SO	SEQUENCE 354 AA; 40339 MW; A70EDSCFAAF7D706 CRC64;			

Query Match 95.9%; Score 1772.5; DB 4; Length 354;  
Best Local Similarity 96.0%; Pred. No. 4e-149;  
Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
QY 1 MNECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCFLFFFSNSLVAIVIKNRK 60
DB 1 MNECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCFLFFFSNSLVAIVIKNRK 60
QY 61 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 120
DB 61 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 120
QY 121 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 180
DB 121 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 180
QY 121 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 180
DB 121 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 180
QY 181 PIYSRSLYFVWVSINLAFLIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 240
DB 181 PIYSRSLYFVWVSINLAFLIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 240
QY 241 VMTVLAFAVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDM 300
DB 241 VMTVLAFAVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDM 300
QY 301 YGTMKKICCFISOE-NPERRSRIPSTVLSRSDTSGOYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKICCFISOE-NPERRSRIPSTVLSRSDTSGOYIEDSISOGAVCNKSTS 353
QY 301 YGTMKKICCFISOE-NPERRSRIPSTVLSRSDTSGOYIEDSISOGAVCNKSTS 353
DB 301 YGTMKKICCFISOE-NPERRSRIPSTVLSRSDTSGOYIEDSISOGAVCNKSTS 353
```

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RESULT 2
Q8VD41 PRELIMINARY; PRT; 194 AA.
AC 08VD41:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Endothelial differentiation G-protein-coupled receptor 7
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L.-Q., Cowles R.A., Logsdon C.D., Mulholland M.W.;
RT LPA Mediates Calcium Signaling in Enteric Glia.
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY013709; AA007694.1;
DR InterPro: IPR005385; EDG7_Receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR004065; LPareceptor.
PFam: PF00001; 7tm_1; 1.
PRINTS: PRO1560; EDG7/RECEPTOR.
PRINTS: PRO0237; GPCR/RHODOPSIN.
DR PRINTS: PRO1527; LPARECEPTOR.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 194
SQ SEQUENCE 194 AA; 22343 MW; 920DICB596F1B8 CRC64;

Query Match 50.3%; Score 929; DB 11; Length 194;
Best Local Similarity 90.2%; Pred. No. 1.4e-74;
Matches 175; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 128 HMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 187
DB 128 HMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 187
QY 188 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 247
DB 188 LVLAVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 247
QY 61 LIFWTVSNLVAFAFIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 120
DB 61 LIFWTVSNLVAFAFIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 120
QY 248 FVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDMYGTMKM 307
DB 248 FVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDMYGTMKM 307
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DB 121 FVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDMYGTMKM 180
QY 308 ICFWQESNPEROPS 194
DB 181 ICFWQESNPEROPS 194

RESULT 3
Q8VD42 PRELIMINARY; PRT; 296 AA.
AC 08VD42:
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 22, Last annotation update)
DE Endothelial differentiation G-protein-coupled receptor 2
DE (Fragment).
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Myenteric plexus;
RA Segura B.J., Xiao L.-Q., Cowles R.A., Logsdon C.D., Mulholland M.W.;
RT LPA Mediates Calcium Signaling in Enteric Glia.
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AY013708; AA007693.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR004065; LPareceptor.
DR PFam: PF00001; 7tm_1; 1.
DR PRINTS: PRO0237; GPCR/RHODOPSIN.
DR PRINTS: PRO1527; LPARECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT NON_TER 296
SQ SEQUENCE 296 AA; 33972 MW; F71EA0267D0275A3 CRC64;

Query Match 48.6%; Score 899; DB 11; Length 296;
Best Local Similarity 54.2%; Pred. No. 9.6e-72;
Matches 162; Conservative 70; Mismatches 63; Indels 4; Gaps 3;

QY 3 ECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCFLFFFSNSLVAIVIKNRK 61
DB 3 ECHYDKHMDFFYNSNTDVTVDWGTGKLVLCVGTFFCFLFFFSNSLVAIVIKNRK 61
QY 1 QCYINESIAFFYNSRSGKYLATENTVSKLYMGL-GITVCIFFMLANLVAIYVYKRRF 58
DB 1 QCYINESIAFFYNSRSGKYLATENTVSKLYMGL-GITVCIFFMLANLVAIYVYKRRF 58
QY 62 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 121
DB 62 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 121
QY 59 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 118
DB 59 HFFPYTYLLANLAADFFAGIAYVFMFNTPVSKITLVNRMFLRQGLDSSLSLSTLNTL 118
QY 122 VIVVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 181
DB 122 VIVVERHMSIMBRVHNSNLTFRKRVTLILLVMAIAIFMGAVPLTGNMNCINISAGSSLA 181
QY 119 ALAIEHITVFRKQILTRMSNRVYVYVIMTAIVGAIPVGMNCIDDIENCSMAP 178
DB 119 ALAIEHITVFRKQILTRMSNRVYVYVIMTAIVGAIPVGMNCIDDIENCSMAP 178
QY 182 IYSRSLYFVWVSINLAFLIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 241
DB 182 IYSRSLYFVWVSINLAFLIMVYVYLRIVYVYKRNLTNLSPTSGSISRRTPMKLMKT 241
QY 179 LYSDSYLVFAINLVYFVYVYVYLAHIFGYVQRTWRMSRHSRGRNRNDTMMSLKTY 238
DB 179 LYSDSYLVFAINLVYFVYVYVYLAHIFGYVQRTWRMSRHSRGRNRNDTMMSLKTY 238
QY 242 MYVLAFAVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDM 300
DB 242 MYVLAFAVVCWTPGLVLLDGLNCGCQVQVHKRWFLLALLNSVYVNIYISKDEDM 300
QY 239 VIVGAFAIICWTPGLVLLD-VCCPCQDVLAWEKFLLAEPNSAMNPIYISYRDKEM 296
DB 239 VIVGAFAIICWTPGLVLLD-VCCPCQDVLAWEKFLLAEPNSAMNPIYISYRDKEM 296

RESULT 4
Q8OF4 PRELIMINARY; PRT; 251 AA.
AC 08OF4:
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
```

DE SC:d22B13.1 (Novel protein similar to lysophosphatidic acid receptor)  
 DE (Fragment).  
 GN SC:d22B13.1.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Babbage A;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC EMBL; AL603747; CAD24409.1; -.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_REC\_P1\_2; 1.  
 DR G-Protein coupled receptor; Receptor; Transmembrane.  
 NON\_TER 1  
 NON\_TER 1  
 SQ SEQUENCE 251 AA; 29076 MW; C4671873B7D5F03 CRC64;  
 Query Match 38.8%; Score 716.5; DB 13; Length 251;  
 Best Local Similarity 51.6%; Pred. No. 1.2e-55;  
 Matches 126; Conservative 60; Mismatches 55; Indels 3; Gaps 2;

QY 3 ECHYDKHDFYNSRNTVDWNG-TKLIVILCVGTFECLIFPNSLVAIAVKRKF 61  
 DB 10 QCYNETAFYNSQKLTATMANAVSKLVGKL-GIVVCIFITLANLVAIYINRF 67  
 QY 62 HPEFYLLANLAADFFAGIAYVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNL 121  
 DB 68 HPIYILMANLAADFFAGIAYVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNL 127  
 QY 122 VIAVERHMSIMRNVHSLTKRVTLLILVMAIIFMGAVPTLGNCLNISACSLAP 181  
 DB 128 AIAERHITVFMQIHTMSNRVYVIVIIWTSIVGALIPSGMNCICADITCSNAP 187  
 QY 182 IYSRSLVFTVNSNMAFLIVVYLRIVYVYKRTNLSPTSGSISRRTPLMTV 241  
 DB 188 LYSNSYLGFMALFNLVTVVVAIHLFMYVYRQRTMRSRSGQRNRDITMSLKT 247  
 QY 242 MVL 245  
 DB 248 VIVL 251.

RESULT 5  
 Q95L85 PRELIMINARY; PRT; 123 AA.  
 AC Q95L85  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Endothelial differentiation gene 7 protein (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang D.-A.; Tiyyl G.; Watsky M.A.;  
 RT "EDG7 of rabbit";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC EMBL; AF04276; AAL01883.1; -.  
 DR InterPro: IPR005385; EDG7\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm1; 1.  
 DR PRINTS: PR01560; EDG7RECEPTOR.

DR PRINTS: PR00237; GPCR\_RHODOPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_REC\_P1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 123 AA; 13883 MW; EB16BAFA7105B65 CRC64;  
 Query Match 32.4%; Score 598; DB 6; Length 123;  
 Best Local Similarity 97.5%; Pred. No. 1.9e-45;  
 Matches 116; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 17 SNTDVTDDMTGKTLIVLCVGTFFCLIFPNSLVAIAVKRKFHFPFYLLANLAAD 76  
 DB 4 SNTDVTDDMTGKTLIVLCVGTFFCLIFPNSLVAIAVKRKFHFPFYLLANLAAD 63  
 QY 77 PFAGIAYVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMR 135  
 DB 64 PFAGIAYVFLMFTGPKSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMR 122

RESULT 6  
 Q9R235 PRELIMINARY; PRT; 382 AA.  
 AC Q9R235  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Lysophospholipid receptor B1.  
 GN EDG1 OR Lpbl.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1295svj;  
 RX MEDLINE=99132320; PubMed=9931453;  
 RA Zhang G., Contos J.J., Weiner J.A., Fukushima N., Chun J.;  
 RT \*Comparative analysis of three murine G-protein coupled receptors  
 RT activated by sphingosine-1-phosphate.\*;  
 RL Gene 227:89-99(1999).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC EMBL; AF108019; AAD16975.1; -.  
 DR MGD; MGI:1096355; Edg1.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004061; S1Preceptor.  
 DR Pfam: PF00001; 7tm1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSN.  
 DR PRINTS: PR01523; S1PRECEPTOR.  
 DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_REC\_P1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 382 AA; 42613 MW; 2EE4B974E9FBE39C CRC64;  
 Query Match 29.7%; Score 548; DB 11; Length 382;  
 Best Local Similarity 34.2%; Pred. No. 1.7e-40;  
 Matches 117; Conservative 79; Mismatches 126; Indels 20; Gaps 7;

QY 27 GTRIVILCVGTFFCLIFPNSLVAIAVKRKFHFPFYLLANLAADFFAGIAYVFL 86  
 DB 44 GIKLSVYFI--LICCFITLLENIIFLITWTKRFRPMYVYIGNLALSDLAGAVAYAN 101  
 QY 87 MENIGPVSKITLVNRMFLROGLDSSLTASLTNLVIAVERHMSIMRNVHSLTKRVT 146  
 DB 102 LILSGATYKLTLPAPMFLREGSMFVALASVSLAIAIERITMLKKLHNGSSSRSF 161  
 QY 147 LILILVMAIIFMGAVPTLGNCLNISACSLATVRSYVFTVNLMAFLMAYVY 206  
 DB 162 LILSACWYISLIGLPSMGWNCISSSCSTVLPDLKHRYLFTCTVFTLLLSIVLY 221  
 QY 207 LRIYVYVRKTNVLSPHTSISRRT--PKLTKVTMTVLGAFVVCWTPGLVLYPLD-G 263

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Db      222 CRIYSLVTRTSRRITFFRNKNSKASRSSEKSLALTKYIIVLSYFIACWAPFLILLDVG 281
QY      264 LNCRCGVQVHKRRFFLLALLNSVYVNPITISYKDEDMYGTMKKMICFSGENPE-----R 318
Db      282 CKAATCDILYKAEYFLVLAIVLNSGTNPITITLTKKERRAFIRIVSCCKPNDGSAGKFK 341
QY      319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISGAVCNKS 351
Db      342 RPI-IPGEMFSRSKSDNSHPQKDDGNPPTIMSGVNSS 382

RESULT 7
ID      09DC35      PRELIMINARY;      PRT;      382 AA.
AC      09DC35;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Endothelial differentiation sphingolipid G-protein-coupled receptor
        1.
        EDG1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Lung;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA      Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA      Kadoita K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole G., Quackenbush J.,
RA      Schiraldi L.M., Staudil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA      Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA      Hayashizaki Y.;
RA      "Functional annotation of a full-length mouse cDNA collection.";
RA      Nature 409:685-690(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: AK004591; BAB23393.1; -.
MGI: MGI:1096355; Edg1.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      InterPro: IPR004061; S1P_receptor.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSN.
DR      PRINTS: PR01523; S1PRECEPTOR.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
SQ      SEQUENCE 382 AA; 42639 MW; 5FE4C9A2BD65CB2A CRC64;

Query Match      29.5%; Score 546; DB 11; Length 382;
Best Local Similarity 34.2%; Pred. No. 2.5e-40;
Matches 117; Conservative 76; Mismatches 127; Indels 20; Gaps 7;

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Db      102 LLLSGATVYKLTTPAQWFLREGSMFVALSAYFSLAIAIRYITMLKMKLHNGSNSRSF 161
QY      147 LLLLVAAIAIFMGAVPTLGMNCINISACSSAPISRSYIVWYVSNIMAFIMVYV 206
Db      162 LLLSACVVISLILGGLIMKNCISLSSCSYVLPYHKHILFCTVFTLLSLIYLY 221
QY      207 LRIYVYVKKRTNVLSPHTSGSISRRT--PMKIMKRYVTVLGAFFVVCWPTGLVVLPLD-G 263
Db      222 CRIYSLVTRTSRRITFFRNKNSKASRSSEKSLALTKYIIVLSYFIACWAPFLILLDVG 281
QY      264 LNCRCGVQVHKRRFFLLALLNSVYVNPITISYKDEDMYGTMKKMICFSGENPE-----R 318
Db      282 CKAATCDILYKAEYFLVLAIVLNSGTNPITITLTKKERRAFIRIVSCCKPNDGSAGKFK 341
QY      319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISGAVCNKS 351
Db      342 RPI-IPGEMFSRSKSDNSHPQKDDGNPPTIMSGVNSS 382

RESULT 8
ID      099NR5      PRELIMINARY;      PRT;      326 AA.
AC      099NR5;
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      EDG1 (Fragment).
GN      EDG1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21082082; PubMed=11214319;
RA      Murphy W.C., Elzirik E., Johnson W.B., Zhang Y.P., Ryder O.A.,
RA      O'Brien S.J.;
RA      "Molecular phylogenetics and the origins of placental mammals.";
RA      Nature 409:614-618(2001).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL: AY011706; AK01975.1; -.
MGI: MGI:1096355; Edg1.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      InterPro: IPR004061; S1P_receptor.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSN.
DR      PRINTS: PR01523; S1PRECEPTOR.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW      G-protein coupled receptor; Receptor; Transmembrane.
FT      NON_TER 1
FT      NON_TER 326
SQ      SEQUENCE 326 AA; 36574 MW; 7B6DF34BD398B1F7 CRC64;

Query Match      29.5%; Score 544.5; DB 11; Length 326;
Best Local Similarity 35.1%; Pred. No. 2.9e-40;
Matches 110; Conservative 75; Mismatches 117; Indels 11; Gaps 5;

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QY      27 GTRIVYLCVGTFFCLFFFSNSLVIAVYKRNKFFPPFYLLANLAADFAGIAYVEL 86
Db      4 GIKLTSVFL--LTCGFIILNFIYLLITKTKFKHPRMYFFIGNLALSDLAGAVATYAN 61
QY      147 LLLLVAAIAIFMGAVPTLGMNCINISACSSAPISRSYIVWYVSNIMAFIMVYV 206
Db      122 LLLSACVVISLILGGLIMKNCISLSSCSYVLPYHKHILFCTVFTLLSLIYLY 181
QY      207 LRIYVYVKKRTNVLSPHTSGSISRRT--PMKIMKRYVTVLGAFFVVCWPTGLVVLPLD-G 263

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DB 182 CRISLVNTRSRRLTPFRNKNISKASRSSKSLALKTIVIVLSVFIACNAPLIFILLIDVVG 241  
QY 264 LNCRCGYQVHKRMFLALLNSVNPPIITYSKDEDMGTMKMICFSGQENPE-----R 318  
DB 242 CKAATCDLTKAEYFLVLAVALNSGTPITITITNEMKRAFRIRYSCCKCPGSDSAGKFK 301  
QY 319 RPSRIPSTVLSRS 331  
DB 302 RPI-IPGMEFSRS 313

RESULT 9

Q92009 PRELIMINARY; PRT; 378 AA.  
AC Q92009;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE LYSPHOSPHOLIPID receptor B3 (Endothelial differentiation).  
LPB3 OR EDG3.  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-129SVJ;  
RX MEDLINE=99132320; PubMed=9931453;  
RA Zhang G., Contos J.J.A., Weiner J.A., Fukushima N., Chun J.;  
RT "Comparative analysis of three murine G-protein coupled receptors  
RL activated by sphingosine-1-phosphate.";  
RN Gene 227:89-99(1999).  
[2]  
RP SEQUENCE FROM N.A.  
RA Ohta K., Wada A., Igarashi Y.;  
RT "Mus musculus sphingosine 1-phosphate receptor Edg3 gene, complete.";  
RN Submitted (May-1999) to the EMBL/Genbank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J; TISSUE=Cerebellum, Head, Lung, and Testis;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";

DR EMBL; AF108021; AAD1697.1; -  
DR EMBL; AB028143; BAA78207.1; -  
DR EMBL; AK028043; BAC25715.1; -  
DR EMBL; AK029852; BAC26645.1; -  
DR EMBL; AK030134; BAC26800.1; -  
DR EMBL; AK047268; BAC33008.1; -  
DR EMBL; AK081919; BAC38373.1; -  
DR EMBL; AK084944; BAC39316.1; -  
DR EMBL; AK085180; BAC39383.1; -  
DR MGI; MGI:1339365; Edg3.  
DR InterPro: IPR000194; Arpase.a/bcentre.  
DR InterPro: IPR004062; EDG3\_receptor.  
DR InterPro: IPR000276; GPCR\_Rhodpsn.  
DR InterPro: IPR004061; S1Preceptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR01524; EDG3RECEPTOR.  
DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
DR PRINTS; PR01523; S1PRECEPTOR.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; 1.  
DR PROSITE; PS00337; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 378 AA; 42270 MW; F46B25E77ECDC8 CRC64;

Query Match 29.4%; Score 543.5; DB 11; Length 378;  
Best Local Similarity 35.2%; Pred. No. 41e-40;  
Matches 123; Conservative 66; Mismatches 123; Indels 37; Gaps 9;

QY 27 GTRIVILCVGTFEFLFEFFNSLVIAVYKRRKFFPPYLLANLAADFPAGIAYVL 86  
DB 39 GRLITITILELVY--CSFYLENLMVLAIAKRNKRNHRYFFIGNALCDLLAGIATKYN 96  
QY 87 MENTGPVSKTLYVNRKFLRQGLDSSLTASLTNLVIAVERMSIRMRHNSLTKRRVT 146  
DB 97 ILMGRKTFRLSPVWFLREGSMFVALGASTCSLIAIAERHLLTMKRPDANKKHRYF 156  
QY 147 LLLILVMAIAIFMGAVPTIGMNCNLSGSSLAIPYSYLVFTVSNLMAFLI-MVYV 205  
DB 157 LILGMCWLAIFSLGALPIIGMNCLENFPCDSTILPLYSKRYIAF-LISIFTAIVTVIL 215  
QY 206 YLRIVVYKRVKTNVSPHTSGSISRRRPVMTKMTVMVYLAGVAVVQWPGVLVPLDGLN 265  
DB 216 YARITICLVKSSRRVANHNS-----ERSMALLRIVVIVSYFIACWSP-LTILFLIDVA 268  
QY 266 CR--OCGYQVHKRMFLALLNSVNPPIITYSKDEDMGTMKMIC-CF-----SOE 314  
DB 269 CKAKECSILFKSQWFTMLAVLNSAMNPVYTLASKEMRRAPFRLVCGCLVKGKGTQASPM 328  
QY 315 NERRRPSRIPSTVLSRSDTGSQYID-----SISGAVC 348  
DB 329 QPALDPSNRKSSSSNNSHSPVKEDLPVATSSCTIDKRSFONGVLC 377

RESULT 10

Q8BP20 PRELIMINARY; PRT; 378 AA.  
AC Q8BP20;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Endothelial differentiation.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J; TISSUE=Mesonephros;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
DR EMBL; AK078443; BAC3727.1; -  
SQ SEQUENCE 378 AA; 42339 MW; F416DBEE7727BDC8 CRC64;

Query Match 29.3%; Score 541.5; DB 11; Length 378;  
Best Local Similarity 35.2%; Pred. No. 6.2e-40;  
Matches 123; Conservative 65; Mismatches 124; Indels 37; Gaps 9;  
QY 27 GTRIVILCVGTFEFLFEFFNSLVIAVYKRRKFFPPYLLANLAADFPAGIAYVL 86  
DB 39 GRLITITILELVY--CSFYLENLMVLAIAKRNKRNHRYFFIGNALCDLLAGIATKYN 96  
QY 87 MENTGPVSKTLYVNRKFLRQGLDSSLTASLTNLVIAVERMSIRMRHNSLTKRRVT 146  
DB 97 ILMGRKTFRLSPVWFLREGSMFVALGASTCSLIAIAERHLLTMKRPDANKKHRYF 156  
QY 147 LLLILVMAIAIFMGAVPTIGMNCNLSGSSLAIPYSYLVFTVSNLMAFLI-MVYV 205  
DB 157 LILGMCWLAIFSLGALPIIGMNCLENFPCDSTILPLYSKRYIAF-LISIFTAIVTVIL 215  
QY 206 YLRIVVYKRVKTNVSPHTSGSISRRRPVMTKMTVMVYLAGVAVVQWPGVLVPLDGLN 265  
DB 216 YARITICLVKSSRRVANHNS-----ERSMALLRIVVIVSYFIACWSP-LTILFLIDVA 268  
QY 266 CR--OCGYQVHKRMFLALLNSVNPPIITYSKDEDMGTMKMIC-CF-----SOE 314  
DB 269 CKAKECSILFKSQWFTMLAVLNSAMNPVYTLASKEMRRAPFRLVCGCLVKGKGTQASPM 328

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OY 315 NPERPRIPSTVLSRSDTGSQYTED-----SISGAVC 348
DB 329 QPALDPSRKSSSSSSNSHSPKVEDLPRVATSSCIIDKNRSFONGVLC 377

RESULT 11
O9DDK4 PRELIMINARY; PRT; 362 AA.
ID Q9DDK4
AC Q9DDK4
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Sphingosine 1-phosphate receptor.
GN EDG1.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;

[1]
SEQUENCE FROM N.A.
RX MEDLINE=20563813; PubMed=11112429;
RA Im D.S., Ungar A.R., Lynch K.R.;
RT "Characterization of a zebrafish (Danio rerio) sphingosine 1-phosphate
RT receptor expressed in the embryonic brain.";
RL Biochem. Biophys. Res. Commun. 279:139-143(2000).
DR EMBL; AF21294; AAC45430.1; -.
DR ZFIN; ZDB-GENE-001228-2; edg1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1PReceptor.
DR Pfam; PF00003; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KM Receptor.
SQ SEQUENCE 362 AA; 40583 MW; 43A398871DA2D9D4 CRC64;

Query Match 29.2%; Score 540.5; DB 13; Length 362;
Best Local Similarity 35.0%; Pred. No. 7.3e-40;
Matches 115; Conservative 68; Mismatches 127; Indels 19; Gaps 6;

OY 41 CLTIFPSNSVIAVTKRKHFFPYLLANLAADFFAGIAYVFLMNTGSPVSKITLVN 100
DB 35 CCEIILENVLTLLTWTKRKHFFPYLLANLAADFFAGIAYVFLMNTGSPVSKITLVN 94
OY 101 RWFRLGGLDSSLTASTLNTLVAVRHMSSIMRVRHNSLTKKRVTLILLVAIAIENG 160
DB 95 QWFFRESMVALAASFSLAIAIERHILTKKLNNGKTCRAVFLISTVWFIAIILG 154
OY 161 AVPLGNCICNISACSLAPIYSRSYLVPTVSNLMAFLIMVVYLVYVYVYKRTNVL 220
DB 155 GLPVMGNCIDISINCSVTPLVHKAYILECTYFESVILMAVILVARIYALVATRSKTL 214
OY 221 -----SPRTSSISRRKTPMLAKTVLVGAFVVCWTPGLVYLPLDLGNCR--QCGVQHV 274
DB 215 VFRKVAAGRSNKSSEKSMALLTIVILVLSCTIACAPLFLILLID--VACQTLTCSITVYK 273
OY 275 KRFMLALATNSVYVNPPIIYSYKDEDMYGTMMKMICCSQENPERPSR-IPSTVLSR--S 331
DB 274 AEFMLALAVNSAMNPILITLTSNEMRAFIKMLNCGVCVQPSGKSRPIMGAEFSKSKS 333
OY 332 DTGSQYIEDS-----ISGAVCNKS 351
DB 334 DNSSHPKDEPYSPRETIYSSGNITSSS 362

RESULT 12
O99NR1 PRELIMINARY; PRT; 326 AA.
ID Q99NR1
AC Q99NR1
DT 01-JUN-2001 (Tremblrel. 17, Created)

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DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE EDG1 (Fragment).
GN EDG1.
OS Heterocephalus glaber (Naked mole-rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Batmyergidae;
OC Heterocephalus.
NCBI_TaxID=10181;

[1]
SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elzirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AY011711; AKR01979.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR004061; S1PReceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PRINTS; PR01523; S1PRECEPTOR.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1
FT TER 326
SQ SEQUENCE 326 AA; 36607 MW; A0716ADF7BF5BA6 CRC64;

Query Match 29.2%; Score 539.5; DB 11; Length 326;
Best Local Similarity 34.0%; Pred. No. 8e-40;
Matches 112; Conservative 77; Mismatches 117; Indels 23; Gaps 6;

OY 27 GTKIVLYCGTFEFLCFFPSNSVIAVTKRKHFFPYLLANLAADFFAGIAYVFL 86
DB 4 GIKLTIVVFI--LICCFIILENVLTLLTWTKRKHFFPYLLANLAADFFAGIAYVFL 61
OY 87 MFNTGSPVSKITLVNRMFLGGLDSSLTASTLNTLVAVRHMSSIMRVRHNSLTKKRV 146
DB 62 LLISGATYTKLTPAQWFLREGSMVALSASFSLAIAIERITMLTKKLNHNSRSR 121
OY 147 LLLILVAIAIFMGAVPLGNCICNISACSLAPIYSRSYLVPTVSNLMAFLIMVVY 206
DB 122 LLISACWVILILGLIPLMGNCISLSQSVTLVHKAYILECTYFVILLALAIYLY 181
OY 207 LRTIVYVYKRTNVLSPRTSSISRRKTP--FMKLAKTVLVGAFVVCWTPGLVYLPLD 263
DB 182 CRTISLVRTSRRTFRKTNISKASRSSEKSLALKTIVILVLSVFIACWAPLFLILLDVG 241
OY 264 LNCRCGVQHVKKRFLMLALATNSVYVNPPIIYSYKDEDMYGTMMKMICCSQENPE-----R 318
DB 242 CKYKTCILYKAEFLVLAIVNSGTNPITLTKRKRRAFIKMLSCCKPMDSTGKIK 301
OY 319 RP-----SRIPSTVLSRSDTGSQYTED 340
DB 302 RPLIAGMEFSR-----SKSDNSHPKQD 324

RESULT 13
O99NR4 PRELIMINARY; PRT; 326 AA.
ID Q99NR4
AC Q99NR4
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE EDG1 (Fragment).
GN EDG1.
OS Hystrix brachyurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Hystriidae; Hystrix.
NCBI_TaxID=143286;

```

[1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE-21082082; PubMed-11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RT O'Brien S.J.;  
 RL "Molecular phylogenetics and the origins of placental mammals.";  
 CC Nature 409:614-618(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: AY011708; AAK01976.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004061; S1Preceptor.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT 326  
 SEQUENCE 326 AA; 36546 MW; 3E66CA765F725BA9 CRC64;

Query Match 29.1%; Score 538; DB 11; Length 326;  
 Best Local Similarity 36.1%; Pred. No. 1.1e-39;  
 Matches 104; Conservative 73; Mismatches 105; Indels 6; Gaps 4;

OY 27 GTKLIVYLCVGTFCFLFFFSNSLVIAVINKRKHPFFVYLLNLAADFPAGIAYVEL 86  
 DB 4 GIKLTIVYF--LICCFILLENVFLVLTWKTKRHRPMYFIGNLALSDLAGAYTAN 61  
 OY 87 MFNTGPVSKTLTVNRKWLPGDLSLTASLTNLVIAVERHMSIMRVRHSNLTAKRYT 146  
 DB 62 LLISGATYKTLTPQWFLREGSMFVALSASFSLALAIERYITMLKMKLNHNSNSRF 121  
 OY 147 LLLILVMAIAFMGAVPILGNCLNCSACSLAPIYSRSYLVFTVSNLMAFLIMVYV 206  
 DB 122 LLISACWVLSILGLPLTGMNCSLSSCTVPLFKHRYTLFCTVFTLLLAIVLY 181  
 OY 207 LRIYVYVYKRNKTNVLSPTSGSISRRT--PMKIMKTVMVIGAFVWCWTPGLVLPD-G 263  
 DB 182 CRYSLVTRSRRLTFKRNISAKSSSEKSLALAKTYIIVLSVFACNAPFLITLLDVG 241  
 OY 264 LNCRCGVQVHYKRWFLALALNSVNPITYSKEDM-YGIMKKKMICC 310  
 DB 242 CKVKTCIDILYKAEFLVALVNSGNPIYTLTNKEMRRAPTRIMSCC 289

## RESULT 14

099N08 PRELIMINARY: PRT; 326 AA.

099N08;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE EDG1 (Fragment).  
 GN EDG1.  
 OS Myocastor coypu (Coypu) (Nutria).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Myocastoridae;  
 OC Myocastor.  
 OX NCBI\_TaxID=10157;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21082082; PubMed-11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RT O'Brien S.J.;  
 RL "Molecular phylogenetics and the origins of placental mammals.";  
 CC Nature 409:614-618(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AY011714; AAK01982.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004061; S1Preceptor.

DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PRINTS: PR01523; S1PRECEPTOR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT 326  
 SEQUENCE 326 AA; 36357 MW; 18963183F9742FF CRC64;

Query Match 29.1%; Score 537.5; DB 11; Length 326;  
 Best Local Similarity 35.4%; Pred. No. 1.2e-39;  
 Matches 102; Conservative 75; Mismatches 106; Indels 5; Gaps 3;

OY 26 TGTKLIVYLCVGTFCFLFFFSNSLVIAVINKRKHPFFVYLLNLAADFPAGIAYVE 85  
 DB 3 SCVKLTIVYF--LICCFILLENVFLVLTWKTKRHRPMYFIGNLALSDLAGAYTAN 60  
 OY 86 IMFNTGPVSKTLTVNRKWLPGDLSLTASLTNLVIAVERHMSIMRVRHSNLTAKRY 145  
 DB 61 NLLSGTYYRLTLVQWFLREGSMFVALSASFSLALAIERYITMLKMKLNHNSNSRF 120  
 OY 146 TLLILVMAIAFMGAVPILGNCLNCSACSLAPIYSRSYLVFTVSNLMAFLIMVYV 205  
 DB 121 FLLISGCAVLSILGLPLTGMNCSLSSCTVPLFKHRYTLFCTVFTLLLAIVLY 180  
 OY 206 YRIYVYVYKRNKTNVLSPTSGSISRRT--PMKIMKTVMVIGAFVWCWTPGLVLPD- 262  
 DB 181 YCRISLVTRSRRLTFKRNISAKSSSEKSLALAKTYIIVLSVFACNAPFLITLLDVG 240  
 OY 263 GLNCRQGVQVHYKRWFLALALNSVNPITYSKEDM-YGIMKKKMICC 310  
 DB 241 GCKVTCIDILYKAEFLVALVNSGNPIYTLTNKEMRRAPTRIMVSC 288

## RESULT 15

09BF65 PRELIMINARY: PRT; 326 AA.

09BF65;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE EDG1 (Fragment).  
 GN EDG1.  
 OS Orycterus afer (Aardvark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.  
 OX NCBI\_TaxID=9818;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21082082; PubMed-11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RT O'Brien S.J.;  
 RL "Molecular phylogenetics and the origins of placental mammals.";  
 CC Nature 409:614-618(2001).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR EMBL: AY011701; AAK01970.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004061; S1Preceptor.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PRINTS: PR01523; S1PRECEPTOR.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1  
 FT 326  
 SEQUENCE 326 AA; 36562 MW; 6946C83C8D79D715 CRC64;

Query Match 29.0%; Score 536; DB 6; Length 326;  
 Best Local Similarity 36.8%; Pred. No. 1.6e-39;  
 Matches 106; Conservative 69; Mismatches 107; Indels 6; Gaps 4;



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: August 18, 2003, 15:09:56 ; Search time 30 Seconds  
(without alignments)  
497.858 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848

Sequence: 1 MNECHYDKHMDFFYRNSNTD.....GSQYIEDSISGAVCNKSTS 353

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Dackfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1848	100.0	353	3	US-08-997-803-14
2	1838	99.5	353	4	US-09-731-030A-16
3	1772.5	95.9	354	3	US-09-325-897-2
4	1772.5	95.9	354	4	US-09-837-726-2
5	995	53.8	213	3	US-08-997-803-15
6	948.5	51.3	364	4	US-09-169-205D-20
7	948.5	51.3	364	4	US-09-731-030A-15
8	946.5	51.2	364	3	US-08-763-938-2
9	944.5	51.1	364	5	PCT-US96-10618-2
10	932.5	50.5	393	5	US-08-861-747-2
11	853.5	46.2	351	3	US-09-169-205D-23
12	849.5	46.0	382	4	US-09-542-733-2
13	843.5	45.6	351	3	US-08-789-982-2
14	843.5	45.6	352	4	US-09-582-200A-13
15	843.5	45.6	352	4	US-08-467-948A-4
16	578.5	31.3	393	3	US-08-467-948A-4
17	546	29.5	382	4	US-09-542-733-2
18	546	29.5	382	4	US-09-169-205D-21
19	541	29.3	383	1	US-08-196-989B-4
20	541	29.3	383	2	US-08-760-936-4
21	541	29.3	383	4	US-09-225-024-4
22	537	29.1	378	3	US-09-082-088-2
23	537	29.1	378	4	US-09-546-117-2
24	537	29.1	378	4	US-09-169-205D-22
25	537	29.1	378	4	US-09-731-030A-18
26	533.5	28.9	381	2	US-08-845-566-3
27	533.5	28.9	381	2	US-08-467-948A-28

28	533.5	28.9	381	3	US-08-852-824-18	Sequence 18, Appl
29	533.5	28.9	381	3	US-08-467-947A-28	Sequence 28, Appl
30	533.5	28.9	381	4	US-09-731-030A-17	Sequence 17, Appl
31	533.5	28.9	381	5	PCT-US96-10618-4	Sequence 4, Appl
32	532	28.8	382	4	US-09-262-477-2	Sequence 4, Appl
33	509.5	27.6	334	1	US-08-118-270-73	Sequence 73, Appl
34	509.5	27.6	334	5	PCT-US93-08528-73	Sequence 73, Appl
35	499	27.0	352	1	US-08-196-989B-2	Sequence 2, Appl
36	499	27.0	352	2	US-08-760-936-2	Sequence 2, Appl
37	499	27.0	352	4	US-09-582-200A-11	Sequence 11, Appl
38	499	27.0	352	4	US-09-169-205D-24	Sequence 24, Appl
39	499	27.0	352	4	US-09-225-024-2	Sequence 2, Appl
40	474.5	25.7	353	4	US-09-582-200A-4	Sequence 4, Appl
41	474.5	25.7	353	4	US-09-582-200A-6	Sequence 6, Appl
42	474.5	25.7	353	4	US-09-582-200A-12	Sequence 12, Appl
43	474.5	25.7	353	4	US-09-731-030A-19	Sequence 19, Appl
44	473.5	25.6	353	4	US-09-582-200A-2	Sequence 2, Appl
45	473.5	25.6	353	4	US-09-582-200A-5	Sequence 5, Appl

## ALIGNMENTS

```
RESULT 1
US-08-997-803-14
; Sequence 14, Application US/08997803
; Patent No. 6057126
;
GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: GUPTA, Ashwani
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejpal B.
; TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixalido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street, N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,803
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wong, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P8074-7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
;
INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
MOLECULE TYPE: protein
US-08-997-803-14

Query Match 100.0%; Score 1848; DB 3; Length 353;
Best Local Similarity 100.0%; Pred.No. 3.5e-151;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNECHYDKHMDFFYRNSNTDVTGTRLVIVLCVGFPCFIFPFSNSLVIAVYIKRK 60
DB 1 MNECHYDKHMDFFYRNSNTDVTGTRLVIVLCVGFPCFIFPFSNSLVIAVYIKRK 60
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QY	61	FHPPFYLLANLAAAEFGIAYVFLMEPTGSVTLVNNMPLRQGLDSSLASATLNL	120
Db	61	FHPPFYLLANLAAAEFGIAYVFLMEPTGSVTLVNNMPLRQGLDSSLASATLNL	120
QY	121	LVIATERHMSIMRVRHNSLTKRKYTLILLWALAIEMGAVPTLGWNCICNISACSSLA	180
Db	121	LVIATERHMSIMRVRHNSLTKRKYTLILLWALAIEMGAVPTLGWNCICNISACSSLA	180
QY	181	PITSRSYLVMTVNSNLMAFLIMVVYVLRIVYVVKRTVLSPHSGSISRRTPMKMT	240
Db	181	PITSRSYLVMTVNSNLMAFLIMVVYVLRIVYVVKRTVLSPHSGSISRRTPMKMT	240
QY	241	VMTVLGAFVVCWTPGILVPLDLGLNCRQGVQVHRKMFLLALLNSVNPILIYSKDEDM	300
Db	241	VMTVLGAFVVCWTPGILVPLDLGLNCRQGVQVHRKMFLLALLNSVNPILIYSKDEDM	300
QY	301	YGTMMKMICCFQSENERBRPSRIPSVYLSRSPGSGOYLIEDTSOGAVCNKETS	353
Db	301	YGTMMKMICCFQSENERBRPSRIPSVYLSRSPGSGOYLIEDTSOGAVCNKETS	353

SULT 2  
 US-09-731-030A-16  
 Sequence 16, Application US/09731030A  
 Patient No. 656096  
 GENERAL INFORMATION:  
 APPLICANT: MUNROE, Donald G  
 APPLICANT: GOPTA, Ashwani K.  
 APPLICANT: ZASTAMNY, Roman L.  
 TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS  
 FILE REFERENCE: 8074-0015  
 CURRENT APPLICATION NUMBER: US/09/7731, 030A  
 CURRENT FILING DATE: 1998-12-29  
 PRIOR APPLICATION NUMBER: 60/070,184  
 PRIOR FILING DATE: 1997-12-30  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 16  
 LENGTH: 353  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG

Query Match	99.5%	Score 1838	DB 4	Length 353
Best Local Similarity	99.7%	Pred. No. 2.5e-150		
Matches 352; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Db	1	MNECHDKHMEFFEYNKSNSTDFVDMGTGTLVTLVCGTFECLFEFFSNLSIAAVIKNRK	60
Qy	61	FHFPEYTLANLAAAFPAJIAVFLFMEPTGVSUPLVYVNHRELBOGLDSSLASLITNL	120
Db	61	FHFPEYTLANLAAAFPAJIAVFLFMEPTGVSUPLVYVNHRELBOGLDSSLASLITNL	120
Qy	121	LVIAVERHMSIMBRVHNSLTKKRYTLTLLVMAAIAIFMGAVPTLGWNCICNISACSSLA	180
Db	121	LVIAVERHMSIMBRVHNSLTKKRYTLTLLVMAAIAIFMGAVPTLGWNCICNISACSSLA	180
Qy	181	PITSRSYLVWVWYNSNLMAPLIMVVVYLRIYVYVKRKTWVLSPHSGSISRRTPMKLMKT	240
Db	181	PITSRSYLVWVWYNSNLMAPLIMVVVYLRIYVYVKRKTWVLSPHSGSISRRTPMKLMKT	240
Qy	241	VMTVLGAFFVVCWTPGLVLPDLGOLNCROCGOVHVRKMFLLALALNSVNPITISYKDEDM	300
Db	241	VMTVLGAFFVVCWTPGLVLPDLGOLNCROCGOVHVRKMFLLALALNSVNPITISYKDEDM	300
Qy	301	YGMKMKUICFSEQENERRRSPRTPSVLRSRDTGSQYIEDTSIQGAVCNKSTKS	353
Db	301	YGMKMKUICFSEQENERRRSPRTPSVLRSRDTGSQYIEDTSIQGAVCNKSTKS	353

RESULT 3  
US-09-325-897-2  
; Sequence 2, Application US/09325897

```

APPLICANT: Ping Tsui
APPLICANT: Catherine E. Ellis
APPLICANT: Ganesh M. Sathe
APPLICANT: Stephanie Van Horn
APPLICANT: Robert S. Ames
APPLICANT: James J. Foley
APPLICANT: Laura R. Fitzgerald
APPLICANT: Harry M. Sarau
APPLICANT: Jonathan K. Chambers
TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR
FILE REFERENCE: GH70014-2
CURRENT APPLICATION NUMBER: US/09/325,897
CURRENT FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 09/215,072
EARLIER FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/992,031
EARLIER FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: 60/046,366
EARLIER FILING DATE: 1997-05-13
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 354
TYPE: PRT
ORGANISM: Human
US-09-325-897-2

```

Query Match	95.9%	Score 1772.5	DB 3	Length 354
Best Local Similarity	96.0%	Pred. No. 1.1e-144		
Matches 340	Conservative	6	Mismatches 7	Indels 1
				Gaps 1

Oy	60	MNECHYKHADPEYNSNTPTVDMDNGTKLYIVLACGTFPCLEIFPSNSLTVAAVYKXNK
Db	1	MNECHYKHADPEYNSNTPTVDMDNGTKLYIVLACGTFPCLEIFPSNSLTVAAVYKXNK
Oy	61	FHPPEYLLANLAAADPEAGIAVYFIMFNTGPVSKTLVYVNRMLROGLDDSLTFASLTJNL
Db	61	FHPPEYLLANLAAADPEAGIAVYFIMFNTGPVSKTLVYVNRMLROGLDDSLTFASLTJNL
Oy	121	LVIVVERHMSIMRMRVNSLTKKRYTLILLVWAIFIPGAVPTLGMNCLCNISACSSIA
Db	121	LVIVVERHMSIMRMRVNSLTKKRYTLILLVWAIFIPGAVPTLGMNCLCNISACSSIA
Oy	121	LVIVVERHMSIMRMRVNSLTKKRYTLILLVWAIFIPGAVPTLGMNCLCNISACSSIA
Db	121	LVIVVERHMSIMRMRVNSLTKKRYTLILLVWAIFIPGAVPTLGMNCLCNISACSSIA
Oy	181	PIYSRSLTVWYVYNSLMAFLIMVYVYLRIVVYKRTNVLSPHTSGSISRRTPKMLMT
Db	181	PIYSRSLTVWYVYNSLMAFLIMVYVYLRIVVYKRTNVLSPHTSGSISRRTPKMLMT
Oy	241	VMYVLGAFVVCMTPLGLVVLPLDGLNCRQCVCVQVHKRMFLLLALNLSVMPPIYSYDEDM
Db	241	VMYVLGAFVVCMTPLGLVVLPLDGLNCRQCVCVQVHKRMFLLLALNLSVMPPIYSYDEDM
Oy	301	YGTAKKATCCFSQE-NPERRPRSLPTSVYLSRSTGSOYIEDTSIGCAVCCNKSTS
Db	301	YGTAKKATCCFSQE-NPERRPRSLPTSVYLSRSTGSOYIEDTSIGCAVCCNKSTS

RESULT 4  
US-09-837-726-2  
; Sequence 2, Application US/09837726

APPLICANT: Tsui, Ping  
APPLICANT: Ellis, Catherine E.  
APPLICANT: Sathé, Ganesh M.  
APPLICANT: Van Horn, Stephanie  
APPLICANT: Ames, Robert A.  
APPLICANT: Foley, James J.

APPLICANT: Fitzgerald, Laura  
 APPLICANT: Sarau, Henry M.  
 TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR  
 FILE REFERENCE: GH-70014-D3  
 CURRENT APPLICATION NUMBER: US/09/837,726  
 PRIOR FILING DATE: 2001-04-18  
 PRIOR APPLICATION NUMBER: 60/046,366  
 PRIOR FILING DATE: 1997-05-13  
 PRIOR APPLICATION NUMBER: 08/992,031  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: 09/215,072  
 PRIOR FILING DATE: 1998-12-18  
 PRIOR APPLICATION NUMBER: 09/325,897  
 PRIOR FILING DATE: 1999-06-04  
 NUMBER OF SEQ ID NOS: 2  
 SOFTWARE: FastSeq for Windows version 3.0  
 SEQ ID NO 2  
 LENGTH: 354  
 TYPE: PRT  
 ORGANISM: HOMO SAPIENS  
 S-09-837-726-2

Query Match 95.9%; Score 1772.5; DB 4; Length 354;  
 Best Local Similarity 96.0%; Pred. No. 1.1e-144;  
 Matches 340; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

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QY 1 MNECHYDHDPEFYRSTNDYDWDGTGRLVYVLCVGFECLEFFFSNLSVIAAVYKNNK 60
DB 1 MNECHYDHDPEFYRSTNDYDWDGTGRLVYVLCVGFECLEFFFSNLSVIAAVYKNNK 60
QY 61 FHPEPYLLANLAADFFAGIAYVFLMNTGVSFVSKTLVYVNWFLRQGLDSSIFLASLNTL 120
DB 61 FHPEPYLLANLAADFFAGIAYVFLMNTGVSFVSKTLVYVNWFLRQGLDSSIFLASLNTL 120
QY 121 LVIAERHMSIMRBMVHNSLTKKRYTLILLIYMAIAIFMGAVPTLGWNCICISACSSIA 180
DB 121 LVIAERHMSIMRBMVHNSLTKKRYTLILLIYMAIAIFMGAVPTLGWNCICISACSSIA 180
QY 181 PIYSRSLVFWTYSNLMFLIMVYVYLRIYVYVKKRTNVLSPHTSGSISRRTPKMKMT 240
DB 181 PIYSRSLVFWTYSNLMFLIMVYVYLRIYVYVKKRTNVLSPHTSGSISRRTPKMKMT 240
QY 241 VWTVLGAFFVWCTPGLVYVPLDGLNCRQCGVQVHRKWFLLALLNSVNPPIIYSKDEDM 300
DB 241 VWTVLGAFFVWCTPGLVYVPLDGLNCRQCGVQVHRKWFLLALLNSVNPPIIYSKDEDM 300
QY 301 YGTAKMTCFSGE-NPERRSRISTYLSRSDTSQYTEDSISGAVCNKSTS 353
DB 301 YGTAKMTCFSGE-NPERRSRISTYLSRSDTSQYTEDSISGAVCNKSTS 353
QY 301 YSTMKMICFSQERNLDRPRLPSTILSRSDTSQYKEDSSOGYVCKNNKS 354
DB 301 YSTMKMICFSQERNLDRPRLPSTILSRSDTSQYKEDSSOGYVCKNNKS 354

```

RESULT 5  
 US-08-997-803-15  
 Sequence 15, Application US/08997803  
 Patent No. 6057126

GENERAL INFORMATION:  
 APPLICANT: CHUN, Jerald J. M.  
 APPLICANT: GUPTA, Ashwani  
 APPLICANT: MUNROE, Donald G.  
 APPLICANT: VITAS, Tejal B.  
 TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS  
 NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP  
 STREET: 655 Fifteenth Street, N.W., Suite 330  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005-5701  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/997,803  
 FILING DATE: 24-DEC-1997  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mong, King L.  
 REGISTRATION NUMBER: 37,500  
 REFERENCE/DOCKET NUMBER: P8074-7020  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 638-5000  
 TELEFAX: (202) 638-4810  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 213 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-997-803-15

Query Match 53.8%; Score 995; DB 3; Length 213;  
 Best Local Similarity 92.7%; Pred. No. 3.6e-78;  
 Matches 190; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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QY 89 NTGPVSKTLTVNRWFLRQGLDSSIFLASLNTLVIAERHMSIMRBMVHNSLTKKRYTL 148
DB 1 NTGPVSKTLTVNRWFLRQGLDSSIFLASLNTLVIAERHMSIMRBMVHNSLTKKRYTL 148
QY 149 ILLVMAIAIFMGAVPTLGWNCICISACSSLAPISRSYLVFWTYSNLMFLIMVYVYR 208
DB 61 ILLVMAIAIFMGAVPTLGWNCICISACSSLAPISRSYLVFWTYSNLMFLIMVYVYR 120
QY 209 IVYVYVKKRTNVLSPHTSGSISRRTPKMKMTVYVGLAFVYVWCTPGLVYVPLDGLNCRQ 268
DB 121 IVYVYVKKRTNVLSPHTSGSISRRTPKMKMTVYVGLAFVYVWCTPGLVYVPLDGLNCRQ 180
QY 269 CGVOHVRKWFLLALLNSVNPPIIY 293
DB 181 CNVQHVYKWFLLALLNSVNPPIIY 205

```

RESULT 6  
 US-09-169-205D-20  
 Sequence 20, Application US/09169205D  
 Patent No. 6485922

GENERAL INFORMATION:  
 APPLICANT: Erikson, James  
 APPLICANT: Goddard, J. Graham  
 APPLICANT: Kieffer, Michael  
 TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE  
 TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR  
 FILE REFERENCE: 252/004  
 CURRENT APPLICATION NUMBER: US/09/169,205D  
 CURRENT FILING DATE: 1998-10-09  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 20  
 LENGTH: 364  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-169-205D-20

Query Match 51.3%; Score 948.5; DB 4; Length 364;  
 Best Local Similarity 51.6%; Pred. No. 6.3e-74;  
 Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;

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QY 1 MNE-CHYDHDPEFYRSTNDYDWDG-TGRLVYVLCVGFECLEFFFSNLSVIAAVYK 57
DB 19 MNEPCFVNESIAFFNRSKHLATEBMVSKLWGL--GIYVCIFIMLANLLVVAIVY 76
QY 58 NRKFPFYLLANLAADFFAGIAYVFLMNTGVSFVSKTLVYVNWFLRQGLDSSIFLASL 117

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Db 77 NRHFPIYIYMANLAAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDISLASV 136  
QY 118 TNLVIAVERHMSIMRMRHSNLTNRKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177  
Db 137 ANLAIATERIHTFRMQLHTRMSNRVAVVIVITWMAIYMGAIIPSGMNCIDIEACS 196  
QY 178 SLATISRSYLVETVSNLMAFLIMVYVYLRIYVYVAKTNVLSPHISGTSRRRTPKL 237  
Db 197 NMAPLVSDSYLVAFIENFLVTFVAVVYLIAHIFGVROTRMRSHSSGPRRNDTMSL 256  
QY 238 MKTYMTVLGAFVVCWPTGLVYVLPDGLNCRQCGVQVHVRKRWFLTLALNSVNPPIYSYKD 297  
Db 257 LKTVIYVIGAFIICWTPGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSAMNPPIYSYRD 315  
QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329  
Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

## RESULT 7

-09-731-030A-15  
Sequence 15, Application US/09731030A  
Patent No. 6566096  
GENERAL INFORMATION:  
APPLICANT: MUNROE, Donald G.  
APPLICANT: GUPTA, Ashwani K.  
APPLICANT: ZASTAWNY, Roman L.  
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS  
FILE REFERENCE: 8074-0015  
CURRENT APPLICATION NUMBER: US/09/731,030A  
PRIOR FILING DATE: 1998-12-29  
PRIOR APPLICATION NUMBER: 60/070,184  
PRIOR FILING DATE: 1997-12-30  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 15  
LENGTH: 364  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG  
US-09-731-030A-15

Query Match 51.3%; Score 948.5; DB 4; Length 364;  
Best Local Similarity 51.6%; Pred. No. 6.3e-74;  
Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;

QY 1 MNE--CHYDKHMDFFNRSNTDVTDDW-TGFKLYIVCYGTFPCFLTFEFSNLYIAVIR 57  
Db 19 MNEQCCYTNESIAFFYRNSGKHLATEMNTVSKLVML--GTTVCIFIMLANLWVAIYV 76  
QY 58 NRKHFPEYIYLANLAAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDISLASV 117  
Db 77 NRHFPIYIYMANLAAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDISLASV 136  
QY 118 TNLVIAVERHMSIMRMRHSNLTNRKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177  
Db 137 ANLAIATERIHTFRMQLHTRMSNRVAVVIVITWMAIYMGAIIPSGMNCIDIEACS 196  
QY 178 SLATISRSYLVETVSNLMAFLIMVYVYLRIYVYVAKTNVLSPHISGTSRRRTPKL 237  
Db 197 NMAPLVSDSYLVAFIENFLVTFVAVVYLIAHIFGVROTRMRSHSSGPRRNDTMSL 256  
QY 238 MKTYMTVLGAFVVCWPTGLVYVLPDGLNCRQCGVQVHVRKRWFLTLALNSVNPPIYSYKD 297  
Db 257 LKTVIYVIGAFIICWTPGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSAMNPPIYSYRD 315  
QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329  
Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

## RESULT 8

US-08-763-938-2  
Sequence 2, Application US/08763938  
Patent No. 6140060  
GENERAL INFORMATION:  
APPLICANT: CHUN, Jeroald J.M.  
APPLICANT: HECHT, Jonathan H.  
TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nikaido, Matmelsstein, Murray and Oram LLP  
STREET: 655 15th Street, N.W., Suite 350 - G St. Lobby  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,938  
FILING DATE: 12-DEC-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: JAHNS, Kristina M.  
REGISTRATION NUMBER: 41,092  
REFERENCE/DOCKET NUMBER: P8074-6018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 364 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-763-938-2

Query Match 51.2%; Score 946.5; DB 3; Length 364;  
Best Local Similarity 51.9%; Pred. No. 9.4e-74;  
Matches 176; Conservative 75; Mismatches 75; Indels 13; Gaps 5;

QY 1 MNE--CHYDKHMDFFNRSNTDVTDDW-TGFKLYIVCYGTFPCFLTFEFSNLYIAVIR 57  
Db 19 MNEQCCYTNESIAFFYRNSGKHLATEMNTVSKLVML--GTTVCIFIMLANLWVAIYV 76  
QY 58 NRKHFPEYIYLANLAAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDISLASV 117  
Db 77 NRHFPIYIYMANLAAADFFAGIAYFLMNTGPNTRLVSTWLNROGLIDISLASV 136  
QY 118 TNLVIAVERHMSIMRMRHSNLTNRKRVTLILVMAIAIPMGAVPTLGNCLNISACS 177  
Db 137 ANLAIATERIHTFRMQLHTRMSNRVAVVIVITWMAIYMGAIIPSGMNCIDIEACS 196  
QY 178 SLATISRSYLVETVSNLMAFLIMVYVYLRIYVYVAKTNVLSPHISGTSRRRTPKL 237  
Db 197 NMAPLVSDSYLVAFIENFLVTFVAVVYLIAHIFGVROTRMRSHSSGPRRNDTMSL 256  
QY 238 MKTYMTVLGAFVVCWPTGLVYVLPDGLNCRQCGVQVHVRKRWFLTLALNSVNPPIYSYKD 297  
Db 257 LKTVIYVIGAFIICWTPGLVLLLD-VCCPQCDVLAYEKFFLLAEFNSAMNPPIYSYRD 315  
QY 298 EDATGTMKMKICFSGQENP-----ERRPSRIPSTVLS 329  
Db 316 KEMSATFROIICCORSENPPTGTEGSDRSASLSLHNTILA 354

## RESULT 9

PCT-US96-10618-2  
Sequence 2, Application PC/TUS9610618



GENERAL INFORMATION:

APPLICANT: Coleman, Roger  
 APPLICANT: Guegler, Karl J.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Bandman, Olga  
 APPLICANT: Selhammer, Jeffrey J.  
 TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/10618  
 FILING DATE: 20-JUN-1996

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,352  
 FILING DATE: 20-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/567,817  
 FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Glaister, Debra J.  
 REGISTRATION NUMBER: 33,888  
 REFERENCE/DOCKET NUMBER: PF-0042 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166

TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 364 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: Rheumatoid Synovium  
 CLONE: 80853

T-US96-10618-2

Query Match 51.1%; Score 944.5; DB 5; Length 364;  
 Best Local Similarity 51.3%; Pred. No. 1.4e-73;  
 Matches 174; Conservative 76; Mismatches 76; Indels 13; Gaps 5;

1 MNE--CHYDKHNDFFYNSNTDTVDW--TGRVLYVLCVGRFFCLFFPSNSLVIAAYIK 57  
 19 MNEPCCFYNESIAEFYNSGKHLATEMNTVSKLVGL--GIIVCJIFIMLANLVVAIVY 76  
 58 NRKHFPPYLLANLAADFFAGIAYVFLMFTGVSSTLYVNRFLROGLDSSLTASL 117  
 77 NRKHFPPYLLANLAADFFAGIAYVFLMFTGVSSTLYVNRFLROGLDSSLTASL 136  
 118 TNLVIAVERHMSINRMVHNSLTKRKYTLTLVMAIAIFGAVPTLGWNCISASCS 177  
 137 ANLAIATIERHTYRMOHLTRMSNRVYVIVATWAIYMGALIPSGWNCICIDENS 196  
 178 SLAPIYSYSLVFTVSNLMAFLINVVYLRIVYVKKRTVNLSPHTSGSISRRTPKML 237  
 197 NNAPYSDSYLFAIFALFVYVYVYLAHIFGVRQRTMRMSRSHSGPRRNDPTMSL 256  
 238 KTVTVTGVGAFVYVCTPGVLYVPLDGLNCRGCGVHVAKRWFLLLALLSVNPIITYSKD 297  
 257 LKTVAIVLGGFLICWTPLVLLILD--VCCPOCDVLAVERKFLLLAEFNSANMPIITYSYD 315

298 EDMSGTKMKMICFSQENP-----ERRSPNIPSTVLS 329  
 316 KEMSAFPRIQLCCQNSENTAPTESDRASSLNTIILA 354

RESULT 10  
 PCT-US96-10618-3

Sequence 3, Application PC/TUS9610618  
 GENERAL INFORMATION:

APPLICANT: Coleman, Roger  
 APPLICANT: Guegler, Karl J.  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Bandman, Olga  
 APPLICANT: Selhammer, Jeffrey J.  
 TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/10618  
 FILING DATE: 20-JUN-1996

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,352  
 FILING DATE: 20-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/567,817  
 FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Glaister, Debra J.  
 REGISTRATION NUMBER: 33,888  
 REFERENCE/DOCKET NUMBER: PF-0042 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166

TELEX:  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 393 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: U18405  
 PCT-US96-10618-3

Query Match 50.5%; Score 932.5; DB 5; Length 393;  
 Best Local Similarity 50.7%; Pred. No. 1.6e-72;  
 Matches 172; Conservative 78; Mismatches 76; Indels 13; Gaps 5;

1 MNE--CHYDKHNDFFYNSNTDTVDW--TGRVLYVLCVGRFFCLFFPSNSLVIAAYIK 57  
 19 MNEPCCFYNESIAEFYNSGKHLATEMNTVSKLVGL--GIIVCJIFIMLANLVVAIVY 76  
 58 NRKHFPPYLLANLAADFFAGIAYVFLMFTGVSSTLYVNRFLROGLDSSLTASL 117  
 77 NRKHFPPYLLANLAADFFAGIAYVFLMFTGVSSTLYVNRFLROGLDSSLTASL 136  
 118 TNLVIAVERHMSINRMVHNSLTKRKYTLTLVMAIAIFGAVPTLGWNCISASCS 177



```

TITLE OF INVENTION: CDNA CLONE HB8CH90 THAT ENCODES
TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,982
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AIG50050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-789-982-2

Query Match      45.6%; Score 843.5; DB 3; Length 351;
Best Local Similarity 50.3%; Pred No. 6.3e-65;
Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1;

OY 1 MNECHYKHMDFEYRNSNTDVTGDKLVIVLCVGFECFLFEFFSNLSVIAAVIKNR 60
DB 4 MGOCYNNETIGFVYNSGKELSSHR-PRDYVVALGLVSVLYLTNLVIAATASNR 62
OY 61 FHFPPYILLANLAADFFAGIAYVFLMNTGVSRTLVNRFLOGLDSSLTASLNL 120
DB 63 FHPITYLLGNLAADLFAGVAYLFLMFTGPRTRALSLEGWFLRQGLDTSLTASVATL 122
OY 121 LVIAYERHMSIMRMVHNSLTKRVTLLILVMAIAIFMGAVPTGWNCLCNISACSSLA 180
DB 123 LAIAVERHRSVAAVQLHSRLPRGRVYMLIVGVMAALGICLIPASHMCLCALDRCSRA 182
OY 181 PIYSRSYLVEFTVSNIMAFLLMVVYVLRITYYVKKRTNVLSPHTSGSISRRTPKIMKT 240
DB 183 PLISRSYLAVALSSLVFLMLVAVYTRIFVYRRVQMAHVSCHPRYRTTILSVKT 242
OY 241 VMTVIGAFVVCWTPGCVLLPLDGLNCRGCGVOHVRKMFLLALLNSVNPPIYSKDEDM 300
DB 243 VIIIGAFVVCWTPGCVLLPLDGLNCRGCGVOHVRKMFLLALLNSVNPPIYSKDEDM 302
OY 301 YGTMKMIC 310
DB 303 RTFRRLCC 312

RESULT 14
US-09-582-200A-13
; Sequence 13, Application US/09582200A
; Patent No. 6482609
; GENERAL INFORMATION:

```

```

APPLICANT: Munroe, Donald G.
APPLICANT: Kamboj, Rajender
APPLICANT: Peters, Diana
APPLICANT: Kooshesh, Fatemeh
APPLICANT: Vyas, Tejpal B.
APPLICANT: Gupta, Ashwani
TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN INFLAMMATORY
FILE REFERENCE: 108074-00002
CURRENT APPLICATION NUMBER: US/09/582,200A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 09/222,995
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: PCT/CA98/01195
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 60/109,885
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/080,610
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 60/070,185
PRIOR FILING DATE: 1997-12-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 352
TYPE: PRT
ORGANISM: human ED6-6 receptor
FEATURE:
NAME/KEY: misc_feature
LOCATION: (352)..(352)
OTHER INFORMATION: "Xaa" represents any amino acid
US-09-582-200A-13

Query Match      45.6%; Score 843.5; DB 4; Length 352;
Best Local Similarity 50.3%; Pred No. 6.3e-65;
Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1;

OY 1 MNECHYKHMDFEYRNSNTDVTGDKLVIVLCVGFECFLFEFFSNLSVIAAVIKNR 60
DB 4 MGOCYNNETIGFVYNSGKELSSHR-PRDYVVALGLVSVLYLTNLVIAATASNR 62
OY 61 FHFPPYILLANLAADFFAGIAYVFLMNTGVSRTLVNRFLOGLDSSLTASLNL 120
DB 63 FHPITYLLGNLAADLFAGVAYLFLMFTGPRTRALSLEGWFLRQGLDTSLTASVATL 122
OY 121 LVIAYERHMSIMRMVHNSLTKRVTLLILVMAIAIFMGAVPTGWNCLCNISACSSLA 180
DB 123 LAIAVERHRSVAAVQLHSRLPRGRVYMLIVGVMAALGICLIPASHMCLCALDRCSRA 182
OY 181 PIYSRSYLVEFTVSNIMAFLLMVVYVLRITYYVKKRTNVLSPHTSGSISRRTPKIMKT 240
DB 183 PLISRSYLAVALSSLVFLMLVAVYTRIFVYRRVQMAHVSCHPRYRTTILSVKT 242
OY 241 VMTVIGAFVVCWTPGCVLLPLDGLNCRGCGVOHVRKMFLLALLNSVNPPIYSKDEDM 300
DB 243 VIIIGAFVVCWTPGCVLLPLDGLNCRGCGVOHVRKMFLLALLNSVNPPIYSKDEDM 302
OY 301 YGTMKMIC 310
DB 303 RTFRRLCC 312

RESULT 15
US-08-467-948A-4
; Sequence 4, Application US/08467948A
; Patent No. 598164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.

```

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1  TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
2  TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
3  NUMBER OF SEQUENCES: 30
4  ADDRESSSEE: STENNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
5  STREET: 1100 NEW YORK AVE., NW, SUITE 600
6  CITY: WASHINGTON
7  STATE: DC
8  COUNTRY: USA
9  ZIP: 20005
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: FLOPPY DISK
12 COMPUTER: IBM PC COMPATIBLE
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PATEPTIN RELEASE #1.0, VERSION #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/467,948A
17 FILING DATE: 06-JUN-1995
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US95/04079
21 FILING DATE: 30-MAR-1995
22 ATTORNEY/AGENT INFORMATION:
23 NAME: STEFFE, ERIC K.
24 REGISTRATION NUMBER: 36,688
25 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: 202-371-2600
28 TELEFAX: 202-371-3540
29 INFORMATION FOR SEQ ID NO: 4:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 393 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 JS-08-467-948A-4

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Query Match	31.3%	Score 578.5	DB 2	Length 393;
Best Local Similarity	44.5%	Pred. No. 4.1e-42;		
Matches 117; Conservative	47;	Mismatches 88;	Indels 11;	Gaps 1;

[illegible]

Search completed: August 18, 2003, 15:19:56  
Job time : 31 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 15:12:14 ; Search time 57 Seconds

(without alignments)  
811.301 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848  
Sequence: 1 MNECHYDKHMDFFYNRSNTD.....GSQYIEDISOGAVCNKSTS 353

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Minimum number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*  
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15: /cgn2\_6/ptoddata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
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17: /cgn2\_6/ptoddata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptoddata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1838	99.5	353	9 US-09-842-316-4	Sequence 4, Appl1
2	1838	99.5	353	10 US-09-731-030A-16	Sequence 16, Appl1
3	1838	99.5	353	10 US-09-971-228-11	Sequence 11, Appl1
4	1838	99.5	353	11 US-09-811-838-6	Sequence 6, Appl1
5	1838	99.5	353	11 US-09-904-099-35	Sequence 35, Appl1
6	1838	99.5	353	12 US-09-953-686-6	Sequence 6, Appl1
7	1838	99.5	353	14 US-10-037-616-25	Sequence 25, Appl1
8	1838	99.5	353	15 US-10-097-340-338	Sequence 338, App
9	1838	99.5	353	15 US-10-225-567A-553	Sequence 553, App
10	1838	99.5	353	16 US-10-228-762-2	Sequence 2, Appl1
11	1692.5	91.6	354	4 US-09-879-225-2	Sequence 2, Appl1
12	1014.5	54.9	220	15 US-10-073-885-80	Sequence 80, Appl1
13	948.5	51.3	364	9 US-09-842-316-3	Sequence 3, Appl1
14	948.5	51.3	364	10 US-09-731-030A-15	Sequence 15, Appl1
15	948.5	51.3	364	10 US-09-971-228-6	Sequence 6, Appl1

16	948.5	51.3	364	11 US-09-811-838-2	Sequence 2, Appl1
17	948.5	51.3	364	11 US-09-904-099-30	Sequence 30, Appl1
18	948.5	51.3	364	12 US-09-953-686-2	Sequence 2, Appl1
19	948.5	51.3	364	14 US-10-037-616-20	Sequence 20, Appl1
20	948.5	51.3	364	15 US-10-225-567A-152	Sequence 152, App
21	948.5	51.3	364	16 US-10-228-762-15	Sequence 15, Appl1
22	849.5	46.0	348	9 US-09-903-799-2	Sequence 2, Appl1
23	849.5	46.0	382	9 US-09-842-316-5	Sequence 5, Appl1
24	849.5	46.0	382	11 US-09-904-099-32	Sequence 32, Appl1
25	849.5	46.0	382	16 US-10-228-762-16	Sequence 16, Appl1
26	843.5	45.6	351	10 US-09-971-228-8	Sequence 8, Appl1
27	843.5	45.6	351	11 US-09-811-838-4	Sequence 4, Appl1
28	843.5	45.6	351	11 US-09-904-099-31	Sequence 31, Appl1
29	843.5	45.6	351	12 US-09-953-686-4	Sequence 4, Appl1
30	843.5	45.6	351	14 US-10-037-616-22	Sequence 22, Appl1
31	843.5	45.6	351	15 US-10-084-507B-23	Sequence 23, Appl1
32	843.5	45.6	351	15 US-10-225-567A-350	Sequence 350, App
33	578.5	31.3	393	15 US-10-024-494-4	Sequence 4, Appl1
34	547	29.6	384	11 US-09-904-099-4	Sequence 4, Appl1
35	546	29.5	382	9 US-09-969-711-2	Sequence 9, Appl1
36	546	29.5	384	11 US-09-904-099-5	Sequence 5, Appl1
37	541.5	29.3	391	11 US-09-904-099-3	Sequence 3, Appl1
38	537	29.1	378	9 US-09-842-316-7	Sequence 7, Appl1
39	537	29.1	378	10 US-09-731-030A-18	Sequence 18, Appl1
40	537	29.1	378	10 US-09-971-228-7	Sequence 7, Appl1
41	537	29.1	378	11 US-09-904-099-2	Sequence 2, Appl1
42	537	29.1	378	14 US-10-037-616-21	Sequence 21, Appl1
43	537	29.1	378	15 US-10-225-567A-239	Sequence 239, App
44	537	29.1	378	16 US-10-228-762-18	Sequence 18, Appl1
45	533.5	28.9	381	9 US-09-827-937A-18	Sequence 18, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-842-316-4  
; Sequence 4, Application US/09842316  
; Patent No. US20020099191A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSTENSIS, Eva  
; APPLICANT: CASSENHUBER, Johann  
; TITLE OF INVENTION: EDG8 RECEPTOR, ITS PREPARATION AND USE  
; FILE REFERENCE: 38005-147  
; CURRENT APPLICATION NUMBER: US/09/842,316  
; CURRENT FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: EP 116589.3  
; PRIOR FILING DATE: 2000-08-01  
; PRIOR APPLICATION NUMBER: EP 108858.2  
; PRIOR FILING DATE: 2000-04-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 353  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-842-316-4

Query Match	Score	DB	Length
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Matches	352	Conservative	0
Mismatches	0	Indels	0
Gaps	0		
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DB	1	MNECHYDKHMDFFYNRSNTDVTGTLVIVLCGFFCLFFFSNSLYAAYIKRK 60	
QY	61	FHEPPYLLIANLAADFFAGIAYVFLMFTGVSSTLVVNRFLRQGLDSSLTASTNL 120	
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DB 301 YGTMKMICFSQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

## RESULT 2

US-09-731-030A-16  
Sequence 16, Application US/09731030A  
Patent No. US20020142375A1  
GENERAL INFORMATION:  
APPLICANT: MUNROE, Donald G.  
APPLICANT: GUPTA, Ashwani K.  
APPLICANT: ZASTANNY, Roman L.  
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS  
FILE REFERENCE: 8074-0015  
CURRENT APPLICATION NUMBER: US/09/731,030A  
CURRENT FILING DATE: 1998-12-29  
PRIOR APPLICATION NUMBER: 60/070,184  
PRIOR FILING DATE: 1997-12-30  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Mammalian EDG  
US-09-731-030A-16

Query Match 99.5%; Score 1838; DB 10; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNECHYKHMDFNRSNTDVTVDWMTGKLYIVLCVGFELFFFSLSVIAAVIKNRK 60  
QY 61 FHFFYYLLANLAADFFAGIAYVFLMNTGVSKTILVNRMPILROGLDSSLTASLTNL 120  
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## RESULT 3

US-09-971-228-11  
Sequence 11, Application US/09971228  
Patent No. US20020155512A1  
GENERAL INFORMATION:  
APPLICANT: Liao, X. Charlene

APPLICANT: Masuda, Esteban  
APPLICANT: Chu, Peter  
APPLICANT: Pardo, Jorge  
APPLICANT: Li, Congfen  
APPLICANT: Zhao, Haoran  
APPLICANT: Jiang, Yingping  
APPLICANT: Rigol Pharmaceuticals, Incorporated  
TITLE OF INVENTION: EDG: Modulators of Lymphocyte Activation and Migration  
FILE REFERENCE: 021044-000310US  
CURRENT APPLICATION NUMBER: US/09/971,228  
CURRENT FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/284,763  
PRIOR FILING DATE: 2001-04-18  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 11  
LENGTH: 353  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: coupled receptor (GPCR) 7 (EDG7)  
US-09-971-228-11

Query Match 99.5%; Score 1838; DB 10; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 FHFFYYLLANLAADFFAGIAYVFLMNTGVSKTILVNRMPILROGLDSSLTASLTNL 120  
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DB 121 LVIAVERHMSIMRKRHSNLTNRKRVTLILLVMAIAIFMGAVPTLGNMCLCNISACSSLA 180  
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DB 301 YGTMKMICFSQENPERRPSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

## RESULT 4

US-09-811-838-6  
Sequence 6, Application US/09811838  
Publication No. US20030027800A1  
GENERAL INFORMATION:  
APPLICANT: Miller, Duane D.  
APPLICANT: Tigyl, Gabore  
APPLICANT: Dalton, James T.  
APPLICANT: Sarder, Vineet M.  
APPLICANT: Elrod, Don B.  
APPLICANT: Xu, Huiqing  
APPLICANT: Baker, Daniel L.  
APPLICANT: Wang, Dean  
APPLICANT: Lillom, Karoly  
APPLICANT: Fischer, David J.  
APPLICANT: Virag, Tamas  
APPLICANT: Nusser, No. US20030027800A1  
TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF  
FILE REFERENCE: 20609/181

;; CURRENT APPLICATION NUMBER: US/09/811.838  
;; CURRENT FILING DATE: 2001-03-19  
;; PRIOR APPLICATION NUMBER: 60/1290,370  
;; PRIOR FILING DATE: 2000-03-17  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 6  
;; LENGTH: 353  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-811-838-6

Query Match 99.5%; Score 1838; DB 11; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIYYVKKRTVLSPHSGSISRRTPKMLKT 240  
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DB 241 VMTVGAFFVCMTPGLVYLPLDGLNCRQCGVOHVAKRMFLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353  
DB 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353

RESULT 5  
US-09-904-099-35  
;; Sequence 35, Application US/09904099  
;; Publication No. US20030119092A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Shankar, Geetha  
;; APPLICANT: Munnung, Jason N  
;; APPLICANT: Spencer, Juliet V  
;; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS  
;; FILE REFERENCE: 10602-013-999  
;; CURRENT APPLICATION NUMBER: US/09/904,099  
;; CURRENT FILING DATE: 2001-07-11  
;; NUMBER OF SEQ ID NOS: 38  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 35  
;; LENGTH: 353  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-904-099-35

Query Match 99.5%; Score 1838; DB 11; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 121 LVIAVERHMSIMRMVHNSLTRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180  
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DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIYYVKKRTVLSPHSGSISRRTPKMLKT 240  
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QY 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353  
DB 301 YGTMMKMICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISQAVCNKSTS 353

RESULT 6  
US-09-953-686-6  
;; Sequence 6, Application US/09953686  
;; Publication No. US20030130237A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Miller, Duane D.  
;; APPLICANT: Tigyl, Gabor  
;; APPLICANT: Dalton, James T.  
;; APPLICANT: Sardar, Vineet M.  
;; APPLICANT: Elrod, Don B.  
;; APPLICANT: Xu, Huiqing  
;; APPLICANT: Baker, Daniel L.  
;; APPLICANT: Wang, Dean  
;; APPLICANT: Lillom, Karoly  
;; APPLICANT: Fischer, David J.  
;; APPLICANT: Nusser, No. US20030130237A1a  
;; TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF  
;; FILE REFERENCE: 20609/183  
;; CURRENT APPLICATION NUMBER: US/09/953,686  
;; CURRENT FILING DATE: 2002-05-21  
;; PRIOR APPLICATION NUMBER: 09/811,838  
;; NUMBER OF SEQ ID NOS: 26  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 6  
;; LENGTH: 353  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-953-686-6

Query Match 99.5%; Score 1838; DB 12; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHDMFEYRNSMTDVTVDWGTGKLYIVLCVGFECFLTFEFSNSLYIAAYIKRK 60  
DB 1 MNECHYDKHDMFEYRNSMTDVTVDWGTGKLYIVLCVGFECFLTFEFSNSLYIAAYIKRK 60  
QY 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSCTLVNRMFLROGLDSSLTASLTNL 120  
DB 61 FHFPYYLLANLAADFFAGIAYVFLMNTGVSCTLVNRMFLROGLDSSLTASLTNL 120  
QY 121 LVIAVERHMSIMRMVHNSLTRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180  
DB 121 LVIAVERHMSIMRMVHNSLTRKRYTLILLVMAIAIFMGAVPTLGMNCLNISACSSIA 180  
QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIYYVKKRTVLSPHSGSISRRTPKMLKT 240  
DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIYYVKKRTVLSPHSGSISRRTPKMLKT 240  
QY 241 VMTVGAFFVCMTPGLVYLPLDGLNCRQCGVOHVAKRMFLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVGAFFVCMTPGLVYLPLDGLNCRQCGVOHVAKRMFLALLNSVNPPIIYSKDEDM 300

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OY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 7
US-10-037-616-25
; Sequence 25, Application US/10037616
; Publication No. US20020123148A1
; GENERAL INFORMATION:
; APPLICANT: English, Denis
; APPLICANT: Kovacs, Richard J.
; APPLICANT: Rizzo, Maria T.
; APPLICANT: Silva, Daniel T.
; TITLE OF INVENTION: Sphingolipid Compositions and Methods for Their Therapeutic Use
; FILE REFERENCE: 7042-119
; CURRENT APPLICATION NUMBER: US/10/037,616
; PRIORITY FILING DATE: 2002-04-19
; PRIORITY FILING DATE: 2000-10-27
; PRIORITY FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 353
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-037-616-25

Query Match          99.5%; Score 1838; DB 14; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60
Db 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60
OY 61 FHPEFYLLANTLAADFFAGIAYVFLMFTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
Db 61 FHPEFYLLANTLAADFFAGIAYVFLMFTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
OY 121 LVIAVERHMSIMMRVNSNLTKKRVTLLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
Db 121 LVIAVERHMSIMMRVNSNLTKKRVTLLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
OY 181 PIYSRSYLVFWYWSNLMALFLIMVYVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
Db 181 PIYSRSYLVFWYWSNLMALFLIMVYVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
OY 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
Db 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
OY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 8
US-10-097-340-338
; Sequence 338, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
```

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; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIORITY FILING DATE: 2002-03-14
; PRIORITY FILING DATE: 2002-07-025
; PRIORITY FILING DATE: 2001-03-14
; PRIORITY FILING DATE: 2001-03-14
; PRIORITY FILING DATE: 2001-09-26
; PRIORITY FILING DATE: 2001-09-26
; PRIORITY FILING DATE: 2001-03-14
; PRIORITY FILING DATE: 2001-03-14
; PRIORITY FILING DATE: 2001-09-26
; PRIORITY FILING DATE: 2001-09-26
; PRIORITY FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 353
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-097-340-338

Query Match          99.5%; Score 1838; DB 15; Length 353;
Best Local Similarity 99.7%; Pred. No. 4e-170;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60
Db 1 MNECHYDKHMDFFYNSNTDTVDWGTGKLIYLCVGTFFCLIFFSNSLVIAVKNRK 60
OY 61 FHPEFYLLANTLAADFFAGIAYVFLMFTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
Db 61 FHPEFYLLANTLAADFFAGIAYVFLMFTGPKVSKITLVNRMFLROGLDSSSLASTLNL 120
OY 121 LVIAVERHMSIMMRVNSNLTKKRVTLLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
Db 121 LVIAVERHMSIMMRVNSNLTKKRVTLLILLVMAAIFMGAVPTLGNCLNISACSSLA 180
OY 181 PIYSRSYLVFWYWSNLMALFLIMVYVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
Db 181 PIYSRSYLVFWYWSNLMALFLIMVYVYLRITYVYKRTNVLSPHTSGSISRRTPMKLMKT 240
OY 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
Db 241 VMTVLGAFVVCWTPGLVVLPLDGLNCRGCGVQHVKKRFFLLALLNSVYVNPITISYKDEDM 300
OY 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353
Db 301 YGTMKMICFSEQENPERRPSRIPSTVLSRSDGSGYIEDSISOGAVCNKSTS 353

RESULT 9
US-10-225-567A-553
; Sequence 553, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Butner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
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;; CURRENT FILING DATE: 2001-12-19  
;; PRIOR APPLICATION NUMBER: 60/257,144  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 2292  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 553  
;; LENGTH: 353  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-225-567A-553

Query Match 99.5%; Score 1838; DB 15; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60  
QY 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
DB 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
QY 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
DB 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
QY 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
DB 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 10  
US-10-228-762-2  
;; Sequence 2, Application US/10228762  
;; Publication No. US20030130493A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Bonini, James A.  
;; APPLICANT: Huang, Ling Yan  
;; APPLICANT: Borowsky, Beth E.  
;; APPLICANT: Salton, John A.  
;; APPLICANT: Wilson, Amy  
;; APPLICANT: Nagorny, Raisa  
;; TITLE OF INVENTION: DNA Encoding Edg7 Receptor  
;; FILE REFERENCE: 58230-a  
;; CURRENT APPLICATION NUMBER: US/10/228,762  
;; CURRENT FILING DATE: 2002-08-26  
;; PRIOR APPLICATION NUMBER: US/09/356,315  
;; PRIOR FILING DATE: 1999-07-19  
;; PRIOR APPLICATION NUMBER: 09/253,998  
;; PRIOR FILING DATE: 1999-02-22  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.0 - beta  
;; SEQ ID NO 2  
;; LENGTH: 353  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-228-762-2

Query Match 99.5%; Score 1838; DB 16; Length 353;  
Best Local Similarity 99.7%; Pred. No. 4e-170;  
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60  
DB 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60

DB 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60  
QY 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
DB 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
QY 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
DB 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
QY 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
DB 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353

RESULT 11  
US-09-879-225-2  
;; Sequence 2, Application US/09879225  
;; Patent No. US20020061558A1  
;; GENERAL INFORMATION:  
;; APPLICANT: LANE, Pamela  
;; APPLICANT: TSUI, Ping  
;; APPLICANT: ELISHOURBAGY, Nabila A.  
;; TITLE OF INVENTION: MOUSE G PROTEIN COUPLED RECEPTOR EDG7  
;; FILE REFERENCE: GP-70706  
;; CURRENT APPLICATION NUMBER: US/09/879,225  
;; CURRENT FILING DATE: 2001-06-12  
;; PRIOR APPLICATION NUMBER: 60/210,926  
;; PRIOR FILING DATE: 2000-06-12  
;; NUMBER OF SEQ ID NOS: 2  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 2  
;; LENGTH: 354  
;; TYPE: PRT  
;; ORGANISM: MUS MUSCULUS  
US-09-879-225-2

Query Match 91.6%; Score 1692.5; DB 9; Length 354;  
Best Local Similarity 91.0%; Pred. No. 5.2e-156;  
Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60  
DB 1 MNECHYDKHMDFFNRSNTDVTVDWMTGKLYIVLCVGTFFCLFIFSSSLVIAAYIKRRK 60  
QY 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
DB 61 FHFPFYLLANLAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLTNL 120  
QY 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
DB 121 LVIAVERMSIMRMRVHNSLTKRRTLLILYMAAIFMGAVPTLGMNCLNISACSSLA 180  
QY 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
DB 181 PIYSRSLVFTVSNLMAFLIMVYVLLRIYVVKRTNVLSPHTSGSISRRTPKLMKT 240  
QY 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
DB 241 VMTVLGAFVVCWTPGLVLLPLDGLNCRCQGVQVHKRMFLALLNSVNPPIIYSKDEDM 300  
QY 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353  
DB 301 YGTMKMKICFSQENPERPRSRIPSTVLSRSDTGSQYIEDSISOGAVCNKSTS 353



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Page 7

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 18, 2003, 14:32:44 ; Search time 23 Seconds

(without alignments)  
721.758 Million cell updates/sec

Title: US-09-581-252-14

Perfect score: 1848

Sequence: 1 MNECHYKHMDFYRNSMTD.....GSQYIEDSIQCAVCKNSTS 353

Scoring table: BLOSUM62

Searched: 127863 seqs, 47026705 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1838	99.5	353 1	EDG7_HUMAN
2	1697.5	91.9	354 1	EDG7_RAT
3	1692.5	91.6	354 1	EDG7_MOUSE
4	955.5	51.7	366 1	LP11_XENLA
5	948.5	51.3	364 1	EDG2_HUMAN
6	947.5	51.3	366 1	LP12_XENLA
7	946.5	51.2	364 1	EDG2_MOUSE
8	932.5	50.5	393 1	EDG2_SHEEP
9	929.5	50.3	364 1	EDG2_BOVIN
10	843.5	45.6	351 1	EDG4_HUMAN
11	839	45.4	351 1	EDG4_MACFA
12	736.5	39.9	348 1	EDG4_MOUSE
13	546	29.5	382 1	EDG1_MOUSE
14	541	29.3	383 1	EDG1_RAT
15	537	29.1	378 1	EDG3_HUMAN
16	533.5	28.9	381 1	EDG1_HUMAN
17	499	27.0	352 1	H218_RAT
18	352	19.0	330 1	GPR3_HUMAN
19	351	19.0	330 1	GPR3_MOUSE
20	347	18.8	472 1	CB1R_MOUSE
21	347	18.8	473 1	CB1R_FELCA
22	347	18.8	473 1	CB1R_MOUSE
23	344	18.6	473 1	CB1R_POEGU
24	344	18.6	473 1	CB1R_TARGR
25	341	18.5	472 1	CB1R_HUMAN
26	340	18.4	468 1	CB1A_FUGRU
27	334	18.1	325 1	MC5R_PANTR
28	329.5	17.8	334 1	MC5R_HUMAN
29	328	17.7	325 1	MC5R_HUMAN
30	327.5	17.7	362 1	GPR6_HUMAN
31	326.5	17.7	334 1	GP12_MOUSE
32	326.5	17.7	334 1	GP12_RAT
33	326.5	17.7	363 1	GPR6_RAT

34	326	17.6	325 1	MC5R_MOUSE	P41149 mus musculu
35	319.5	17.3	432 1	MC4R_PIG	O97504 sus scrofa
36	318.5	17.2	370 1	CB1B_FUGRU	O98895 fuqu rubrip
37	314.5	17.0	332 1	MC4R_HUMAN	P32245 homo sapien
38	314	17.0	325 1	MC5R_SHEEP	P41983 homo sapien
39	312	16.9	325 1	MC5R_RAT	P35345 ratu
40	310	16.8	325 1	MC5R_BOVIN	P56451 bos taurus
41	307.5	16.6	332 1	MC4R_BOVIN	O94198 bos taurus
42	302.5	16.4	180 1	EDG5_MOUSE	P52592 mus musculu
43	299.5	16.2	332 1	MC3R_RAT	P70596 ratu
44	295	16.0	323 1	MC3R_MOUSE	P33033 mus musculu
45	294	15.9	390 1	SH1B_HUMAN	P28222 homo sapien

## ALIGNMENTS

RESULT 1  
EDG7\_HUMAN STANDARD; PRT; 353 AA.  
AC O9UB5;  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3).  
GN EDG7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-T-cell;  
RX MEDLINE=99419064; PubMed=10488122;  
RA Bando K., Aoki J., Hosono H., Kobayashi S., Kobayashi T.,  
Muraakami-Murotoshi K., Tsujimoto M., Arai H., Inoue K.;  
RT Molecular cloning and characterization of a novel human G-protein-  
coupled receptor, EDG7, for lysophosphatidic acid.;  
J. Biol. Chem. 274:27776-27785(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Embryonic Kidney;  
RX MEDLINE=20193876; PubMed=10727522;  
RA Im D.-S., Heise C.E., Harding M.A., George S.R., O'Dowd B.F.,  
Theodorescu D., Lynch K.R.;  
RT Molecular cloning and characterization of a lysophosphatidic acid  
receptor, Edg-7, expressed in prostate.;  
Mol. Pharmacol. 57:753-759(2000).  
RN [3]  
RP REVIEW.  
RX MEDLINE=20545693; PubMed=11093753;  
RA Contos J.J.A., Ishii I., Chun J.;  
RT "Lysophosphatidic acid receptors";  
Mol. Pharmacol. 58:1188-1196(2000).  
CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of  
diverse cellular activities. May play a role in the development of  
ovarian cancer. Seems to be coupled to the G(i1)/G(o) and G(q)  
families of heteromeric G proteins.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Most abundantly expressed in prostate, testes,  
pancreas, and heart, with moderate levels in lung and ovary. No  
detectable expression in brain, placenta, liver, skeletal muscle,  
kidney, spleen, thymus, small intestine, colon, or peripheral  
blood leukocytes.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation-  
the European Bioinformatics Institute. There are no restrictions on its  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC -----
DR EMBL: AF127138; AAF05311.1; -
DR EMBL: AF186380; AAF00530.1; -
DR Genew: HGNC:14298; EDG7.
DR MIM: 605106; -
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0008289; F: lipid binding activity; TAS.
DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
DR GO: GO:0007187; P: G-protein signaling, coupled to cyclic nucl. . . ; TAS.
DR GO: GO:0007268; P: synaptic transmission; TAS.
DR InterPro: IPR005385; EDG7_receptor.
DR InterPro: IPR00276; GPCR_rhodopsin.
DR InterPro: IPR004065; LPAR_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1560; EDG7RECEPTOR.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PRO1527; LPARRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lipoprotein; Palmitate.
DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
TRANSMEM 32 52 1 (POTENTIAL).
TRANSMEM 53 67 CYTOPLASMIC (POTENTIAL).
TRANSMEM 68 88 2 (POTENTIAL).
TRANSMEM 89 101 EXTRACELLULAR (POTENTIAL).
TRANSMEM 102 124 3 (POTENTIAL).
TRANSMEM 125 146 CYTOPLASMIC (POTENTIAL).
TRANSMEM 147 167 4 (POTENTIAL).
TRANSMEM 168 186 EXTRACELLULAR (POTENTIAL).
TRANSMEM 187 207 5 (POTENTIAL).
TRANSMEM 208 240 CYTOPLASMIC (POTENTIAL).
TRANSMEM 241 261 6 (POTENTIAL).
TRANSMEM 262 276 EXTRACELLULAR (POTENTIAL).
TRANSMEM 277 297 7 (POTENTIAL).
TRANSMEM 298 353 CYTOPLASMIC (POTENTIAL).
DOMAIN 309 309 CYTOPLASMIC (BY SIMILARITY).
LIPID 15 15 PALMITATE (BY SIMILARITY).
CARBOHYD 172 172 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SEQUENCE 353 AA; 40128 MW; 105DC9DD185E2CE7 CMC64;

Query Match 99.5%; Score 1838; DB 1; Length 353;
Best Local Similarity 99.7%; Pred. No. 5.4e-123;
Matches 352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNECHYDKHMEDEFYRNSNTDVTDMTGTKIVLCVSTFECFLTFEFSNSLVIAAVIKNRK 60
DB 1 MNECHYDKHMEDEFYRNSNTDVTDMTGKIVLCVSTFECFLTFEFSNSLVIAAVIKNRK 60
DB 61 FHPFFYLLANLAADFPAGIAYFLFNFPGVSKTILVNWFRLROGLDSSLTASLTNL 120
DB 61 FHPFFYLLANLAADFPAGIAYFLFNFPGVSKTILVNWFRLROGLDSSLTASLTNL 120
QY 121 LVIVERRHMSIMRRVNSNLTKRKRVTLILLVMAIAFMGAIVPLTGNWCLNISACSSIA 180
DB 121 LVIVERRHMSIMRRVNSNLTKRKRVTLILLVMAIAFMGAIVPLTGNWCLNISACSSIA 180
QY 181 PIYSRSYLVTWYSNLAFLIMVVYLRIYVYVKKRTNVLSPHTSGSISRRRTPMKLMKT 240
DB 181 PIYSRSYLVTWYSNLAFLIMVVYLRIYVYVKKRTNVLSPHTSGSISRRRTPMKLMKT 240
QY 241 VMTVLGAFVVCWMTGLVVLPLDGLNCRQCGVQHKRKFLLALLNSVNPPIIYSKEDM 300
DB 241 VMTVLGAFVVCWMTGLVVLPLDGLNCRQCGVQHKRKFLLALLNSVNPPIIYSKEDM 300
QY 301 YGTAKKMICFSENPERRPSRIPISTVLSRSDTGSOTIEDISOGAVCNKSTS 353
DB 301 YGTAKKMICFSENPERRPSRIPISTVLSRSDTGSOTIEDISOGAVCNKSTS 353
ID EDG7_RAT STANDARD; PRT; 354 AA.

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AC Q9K5ED; Q9ESJ6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3)
DE (snpPCR32).
GN Edg7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Higashioaka M., Mori K.;
RT "Molecular cloning of the rat Edg7 protein and its identification as a
RL functional cellular receptor for lysophosphatidic acid.";
RN Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
[2]
RN SEQUENCE OF 8-354 FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RT "Identification and characterization of novel G-protein coupled
RL receptors expressed in regenerating peripheral nerve.";
CC Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
CC diverse cellular activities. Seems to be coupled to the G(1)/G(0)
CC and G(q) families of heteromeric G proteins (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AB051164; BAB91247.1; -
DR EMBL: AF097733; AAG24262.1; ALT INIT.
DR InterPro: IPR005385; EDG7_receptor.
DR InterPro: IPR00276; GPCR_rhodopsin.
DR InterPro: IPR004065; LPAR_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1560; EDG7RECEPTOR.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PRINTS: PRO1527; LPARRECEPTOR.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate.
DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
TRANSMEM 32 52 1 (POTENTIAL).
TRANSMEM 53 67 CYTOPLASMIC (POTENTIAL).
TRANSMEM 68 88 2 (POTENTIAL).
TRANSMEM 89 101 EXTRACELLULAR (POTENTIAL).
TRANSMEM 102 124 3 (POTENTIAL).
TRANSMEM 125 146 CYTOPLASMIC (POTENTIAL).
TRANSMEM 147 167 4 (POTENTIAL).
TRANSMEM 168 186 EXTRACELLULAR (POTENTIAL).
TRANSMEM 187 207 5 (POTENTIAL).
TRANSMEM 208 240 CYTOPLASMIC (POTENTIAL).
TRANSMEM 241 261 6 (POTENTIAL).
TRANSMEM 262 276 EXTRACELLULAR (POTENTIAL).
TRANSMEM 277 295 7 (POTENTIAL).
TRANSMEM 296 354 CYTOPLASMIC (POTENTIAL).
DOMAIN 309 309 PALMITATE (BY SIMILARITY).
LIPID 15 15 N-LINKED (GLCNAC. . . ) (POTENTIAL).
CARBOHYD 172 172 N-LINKED (GLCNAC. . . ) (POTENTIAL).
CONFLICT 74 74 A -> V (IN REF. 2).
SEQUENCE 354 AA; 40286 MW; 3536C8FA6EC59286 CMC64;

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Query Match 91.9%; Score 1697.5; DB 1; Length 354;  
 Best Local Similarity 91.0%; Pred. No. 4.4e-113;  
 Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFECFLIFPFSNSLYIAAYTKRK 60  
 DB 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFECFLIFPFSNSLYIAAYTKRK 60  
 QY 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120  
 DB 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120  
 QY 121 LVIAVERHMSIMRMRVHNSLTKKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180  
 DB 121 LVIAVERHMSIMRMRVHNSLTKKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180  
 QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIVYVYKRTVLSPHSGSISRRTPKLMKT 240  
 DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIVYVYKRTVLSPHSGSISRRTPKLMKT 240  
 QY 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIYSKDEDM 300  
 DB 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIYSKDEDM 300  
 QY 301 YGTAKMKICFSQF-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353  
 DB 301 YGTAKMKICFSQF-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353

RESULT 3  
 EDG7\_MOUSE STANDARD; PRT; 354 AA.  
 AC Q9E031;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysophosphatidic acid receptor Edg-7 (LPA receptor 3) (LPA-3).  
 GN Edg7 OR LPA3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SvJ, and Swiss Webster / NIH;  
 RX MEDLINE=21213908; PubMed=11313151;  
 RA Cortos J.J.A., Chun J.;  
 RT "The mouse Lp(A3)/Edg7 lysophosphatidic acid receptor gene: genomic structure, chromosomal localization, and expression pattern.";  
 L Gene 267:243-253(2001).  
 RN [2]  
 RP ERRATUM.  
 RA Cortos J.J.A., Chun J.;  
 RL Gene 272:345-345(2001).  
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of diverse cellular activities. Seems to be coupled to the G(1)/G(0) and G(q) families of heteromeric G proteins.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Most abundantly expressed in testes, kidney, and lung, with moderate levels in small intestine, and low levels in heart, stomach, spleen, and adult and perinatal brain. Little or no expression in embryonic brain, liver, or thymus.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL; AF293845; AAG13674.1; .

DR EMBL; AF272365; AK02017.1; .  
 DR EMBL; AF272364; AK02017.1; JOINED.  
 DR MGD; MGI:1929469; Edg7.  
 DR InterPro: IPR005385; Edg7\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004065; LPAreceptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR01560; EDG7RECEPTOR.  
 DR PRINTS; PR02337; GPCR\_RHODOPSIN.  
 DR PRINTS; PR01527; LPAARECEPTOR.  
 DR PROSITE; PS00237; G\_PROTEIN\_REC\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_REC\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Lipoprotein; Palmitate.  
 FT DOMAIN 1 31  
 FT TRANSMEM 32 52  
 FT TRANSMEM 53 67  
 FT TRANSMEM 68 88  
 FT TRANSMEM 89 101  
 FT TRANSMEM 102 124  
 FT TRANSMEM 125 146  
 FT TRANSMEM 147 167  
 FT TRANSMEM 168 186  
 FT TRANSMEM 187 207  
 FT TRANSMEM 208 240  
 FT TRANSMEM 241 261  
 FT TRANSMEM 262 276  
 FT TRANSMEM 277 295  
 FT TRANSMEM 296 354  
 FT DOMAIN 309 309  
 FT CARBOHYD 15 15  
 FT CARBOHYD 172 172  
 SQ SEQUENCE 354 AA; 40315 MW; 8B6F9A3CA9C1F062 CRC64;

Query Match 91.6%; Score 1692.5; DB 1; Length 354;  
 Best Local Similarity 91.0%; Pred. No. 9.9e-113;  
 Matches 322; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFECFLIFPFSNSLYIAAYTKRK 60  
 DB 1 MNECHYDRHDFEYRNSNTDVTVDWGTGKLVIVLCVGFECFLIFPFSNSLYIAAYTKRK 60  
 QY 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120  
 DB 61 FHFFPYLLANLAAADFFAGIAYVFLMNTGVSRTLVNRMFLRQGLDSSLTASLNL 120  
 QY 121 LVIAVERHMSIMRMRVHNSLTKKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180  
 DB 121 LVIAVERHMSIMRMRVHNSLTKKRTLLILVMAIAIFMGAVPTLGMNCLNISACSSLA 180  
 QY 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIVYVYKRTVLSPHSGSISRRTPKLMKT 240  
 DB 181 PIYSRSYLVFTVSNLMAFLIMVYVYLRIVYVYKRTVLSPHSGSISRRTPKLMKT 240  
 QY 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIYSKDEDM 300  
 DB 241 VMTVLGAFVVCWTPGLVYVLPDLGNCRCQGVQHVYKRWFLLLALLNSVNPPIYSKDEDM 300  
 QY 301 YGTAKMKICFSQF-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353  
 DB 301 YGTAKMKICFSQF-NPERRPSRIPSTVLSRDSQYIEDSISOGAVCNKSTS 353

RESULT 4  
 LP11\_XENLA STANDARD; PRT; 366 AA.  
 AC Q9P017;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lysophosphatidic acid receptor LPA1 homolog 1 (XLPAL-1).  
 GN LPA1R1 OR LPA1R.  
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2126767; PubMed=11278944;  
 RA Kimura Y., Schmitt A., Fukushima N., Ishii I., Kimura H.,  
 RA Nedreda A.R., Chun J.;  
 RT "Two novel xenopus homologs of mammalian LPA1/EDG-2 function as  
 RT lysophosphatidic acid receptors in Xenopus oocytes and mammalian  
 RT cells";  
 RL J. Biol. Chem. 276:15208-15215(2001).  
 CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of  
 CC diverse cellular activities. Probably coupled to the activation of  
 CC the G(q) type of heteromeric G proteins, which activates the  
 CC phospholipase C mediated signaling cascade.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed at high levels in oocytes and at  
 CC lower levels in brain and spinal cord. Below detection level in  
 CC lung, heart, kidney, liver, muscle, stomach, and intestine.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: AJ249843; CAB62282.1; -  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR InterPro: IPR004055; LPAR\_receptor.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHOPOPSN.  
 DR PRINTS: PR01527; LPARRECEPTOR.  
 DR PROSITE: PS00237; G-PROTEIN\_RECPT\_P1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECPT\_P1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Lipoprotein; Palmitate.  
 FT DOMAIN 1 55  
 FT TRANSSEM 56 76  
 FT DOMAIN 77 88  
 FT TRANSSEM 89 109  
 FT DOMAIN 110 122  
 FT TRANSSEM 123 145  
 FT DOMAIN 146 165  
 FT TRANSSEM 166 186  
 FT DOMAIN 187 207  
 FT TRANSSEM 208 228  
 FT DOMAIN 229 261  
 FT TRANSSEM 262 282  
 FT DOMAIN 283 290  
 FT TRANSSEM 291 313  
 FT DOMAIN 314 366  
 FT LIPID 329 329  
 FT CARBOHYD 29 29  
 FT CARBOHYD 37 37  
 SO SEQUENCE 366 AA; 41363 MW; 2F5661BD13DCAEE CRC64;

Query Match 51.78; Score 955.5; DB 1; Length 366;  
 Best Local Similarity 51.28; Pred. No. 1e-60;  
 Matches 172; Conservative 79; Mismatches 74; Indels 11; Gaps 4;

2 NECHYDHDHDFNRSNTDVTVDWTG-TKLYIVICVFTEFCIFFSNSIVIAVITNRK 60  
 24 SCQYNTTIAFFYNRSGKYATLATEMNAVSKLWVG--GIVYCFMLANLMAVIAVITNR 81  
 61 FHFPFYLLANLAADFAAGIAYVFLMNTGPKVSKTLVNRWFLROGLDLSLSTASTNL 120  
 82 FHFPFYLLANLAADFAAGIAYVFLMNTGPKVSKTLVNRWFLROGLDLSLSTASTNL 141

QY 121 LVIAVERHMSIMRNRVSHNLTKRKRYTLLILMLMAIAFMGAVPLTGNCLNISACSSLA 180  
 DB 142 LAIAIERHITVEFRQLTRMSNRVRVYIVYIMVIAFMGAIPIGVNMCIDLEQCSMA 201  
 QY 181 PIYRSIVLWTVSNLMAFLIMVYVYLYRIYVYKRNIVLSPIHSGISRRRTPKMLKT 240  
 DB 202 PLYSDSYLIETITNLTVFVNVVLYAHIFVYVYKQRMKSRSHSGRRNDDTMSDLKT 261  
 QY 241 VMTVLGAFVVCQTEGLVPLPDGLNCQCGQVHQHKEWFLILLALNSVNPITYSKDEDM 300  
 DB 262 VVIVLGAIFYCMTIGVILLILD-ICFCPCNLAIEKEFFLLAEKNSANPLITYSKDEM 320  
 QY 301 YGTMKMKICFSGQEN-----PERRPSRIPSTYLS 329  
 DB 321 SATFKQLICQRTENVNGPTEGSDRSASLWHTILA 356

RESULT 5  
 EDG2\_HUMAN STANDARD; PRT; 364 AA.  
 AC 092633; 000656; 000722; P78351;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 26-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1).  
 GN EDG2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97224397; PubMed=9070858;  
 RA An S., Dickens M.A., Bleu T., Hallmark O.G., Goetzl E.J.;  
 RT "Molecular cloning of the human Edg2 protein and its identification  
 RT as a functional cellular receptor for lysophosphatidic acid";  
 RL Biochem. Biophys. Res. Commun. 231:619-622(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97224241; PubMed=9069262;  
 RA Moolenaar W.H., Krenenburg O., Postma F.R., Zondag G.C.M.;  
 RT "Lysophosphatidic acid: G-protein signalling and cellular responses";  
 RL Curr. Opin. Cell Biol. 9:168-173(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RT TISSUE=Hippocampus, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gundaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP REVIEW.  
 RX MEDLINE=20545693; PubMed=11093753;  
 RA Contos J.J.A., Ishii I., Chun J.;  
 RT "Lysophosphatidic acid receptors";  
 RL Mol. Pharmacol. 58:1188-1196(2000).



```

CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
CC diverse cellular activities. Seems to be coupled to the G(1)/G(0),
CC G(12)/G(13), and G(4) families of heteromeric G proteins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in many adult organs, including
CC brain, heart, colon, small intestine, placenta, prostate, ovary,
CC pancreas, testes, spleen, skeletal muscle, and kidney. Little or
CC no expression in liver, lung, thymus, or peripheral blood
CC leukocytes.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; U08081; AAC51139.1; -
DR EMBL; Y09479; CAI70686.1; -
DR EMBL; Y09479; CAI70686.1; -
DR EMBL; U78192; AAC00530.1; -
DR EMBL; BC030615; AAH30615.1; -
DR EMBL; BC036034; AAH36034.1; -
DR PIR; JCS293; JCS293.
DR Genew; HGNC:3166; EDG2.
DR MIM; 602282; -
DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
DR GO; GO:0007204; P:Cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; TAS.
DR GO; GO:0007202; P:phospholipase C activation; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004065; LPAREceptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01527; LPARECEPTOR.
DR PROSITE; PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_REC_P1_2; 1.
DR KX MultiGene family: Lipoprotein; Palmitate;
KV Glycoprotein; Transmembrane; Glycoprotein;
KV MultiGene family: Lipoprotein; Palmitate.
FT DOMAIN 1 50
FT TRANSMEM 51 75
FT TRANSMEM 76 82
FT TRANSMEM 83 111
FT TRANSMEM 112 125
FT TRANSMEM 126 144
FT TRANSMEM 145 163
FT TRANSMEM 164 189
FT TRANSMEM 190 205
FT TRANSMEM 206 226
FT TRANSMEM 227 258
FT TRANSMEM 259 280
FT TRANSMEM 281 294
FT TRANSMEM 295 315
FT TRANSMEM 316 364
FT LIPID 327 327
FT CARBOHD 27 27
FT CARBOHD 35 35
FT CONFLICT 340 340
FT SEQUENCE 364 AA: 41109 MW: 4CA6262FD00DE74 CRC64;

Query Match 51.3%; Score 948.5; DB 1; Length 364;
Best Local Similarity 51.6%; Pred. No. 3,2e-60;
Matches 175; Conservative 76; Mismatches 75; Indels 13; Gaps 5;

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OY 118 TNLIVAEHRHNSIMRVRYSNITKRYTLTLLVWALAEFGAVPTLGMCLNISACS 177
DB 137 ANLVAIAERHTTVERMOLHTKMSRRVYVIVTVAIVGALIPSVGMNICIENS 196
OY 178 SLAPISNSYLVFWTNSIMAEFLINVVYLRIVYVKKRVNLSPTSGSISRRTPKML 237
DB 197 NNAPLYSDSYLVFWMAIFNLVTFVVVLYAHIFGVROKTRMSRRSSGPRRRDMMSL 256
OY 238 KTVTVTGVAFVVCPTPGVYVPLDGLNCRGCVGVKRWELLALNSVNPITYSYD 297
DB 257 LKTVVIVGAFTICPTPGVILLLD-VCCPQCDVLAVERFLLAEFNSAMPITYSYD 315
OY 298 EDMYGTMRKMICFSQENP-----ERRPRIPSTVLS 329
DB 316 KEMSNTPFIQILCCQSENPTGPTBSDRSASSLNTIILA 354

RESULT 6
ID LP12_XENLA STANDARD: PRT: 366 AA.
AC 09PUL6;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Lysophosphatidic acid receptor LPAL homolog 2 (xLPAL-2).
GN LPALR2 OR LPALR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21226767; PubMed-11278944;
RA Kimura Y., Schmitt A., Fukushima N., Ishii I., Kimura H.,
RA Nebreda A.R., Chun J.;
RT "Two novel Xenopus homologs of mammalian LPAL/EDG-2 function as
RT lysophosphatidic acid receptors in Xenopus oocytes and mammalian
RT cells."
RL J. Biol. Chem. 276:15208-15215(2001).
CC -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of
CC diverse cellular activities. Probably coupled to the activation of
CC the G(4) type of heteromeric G proteins, which activates the
CC phospholipase C mediated signaling cascade.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed at high levels in oocytes and at
CC lower levels in brain and spinal cord. Below detection level in
CC lung, heart, kidney, liver, muscle, stomach, and intestine.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; AJ249844; CAB62283.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004065; LPAREceptor.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01527; LPARECEPTOR.
DR PROSITE; PS00237; G-PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_REC_P1_2; 1.
DR KX MultiGene family: Lipoprotein; Palmitate;
KV Glycoprotein; Transmembrane; Glycoprotein;
KV MultiGene family: Lipoprotein; Palmitate.
FT DOMAIN 1 55
FT TRANSMEM 56 76
FT TRANSMEM 77 88
FT TRANSMEM 89 109
FT SEQUENCE 109 AA: 2 (POTENTIAL).

```



cells of the peripheral nervous system. Expressed in many other tissues, including testes, lung, heart, intestine, spleen, kidney, thymus, and stomach. No expression in liver.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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-----

DR EMBL: U70622; AAC52923.1; -

DR EMBL: U48235; AAC53035.1; -

DR EMBL: AF075456; AAC34301.1; -

DR EMBL: AF075453; AAC34301.1; JOINED.

DR EMBL: AF075455; AAC34301.1; JOINED.

DR EMBL: AF075456; AAC34302.1; -

DR EMBL: AF075455; AAC34302.1; JOINED.

DR EMBL: BC025425; AAB25425.1; -

DR EMBL: AF014418; AAB6381.1; -

DR EMBL: AF090347; AAG24469.1; -

DR MGI: 108429; Edg2.

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR InterPro: IPR004065; LPARreceptor.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_RHODOPSIN.

DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.

DR PROSITE: PS0262; G-PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Lipoprotein; Palmitate; Alternative splicing.

FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 51 75 1 (POTENTIAL).

FT TRANSMEM 76 82 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 83 111 2 (POTENTIAL).

FT TRANSMEM 112 125 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 126 144 3 (POTENTIAL).

FT TRANSMEM 145 163 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 164 189 4 (POTENTIAL).

FT TRANSMEM 190 205 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 226 5 (POTENTIAL).

FT TRANSMEM 227 258 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 259 280 6 (POTENTIAL).

FT TRANSMEM 281 294 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 295 315 7 (POTENTIAL).

FT TRANSMEM 316 364 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 327 364 PALMITATE (BY SIMILARITY).

FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 1 18 Missing (in isoform 2).

FT FTID-VSP\_001986.

FT CONFLICT 119 119 S->N (IN REF. 3).

FT CONFLICT 181 183 IPS->MPT (IN REF. 3).

FT CONFLICT 225 225 Y->S (IN REF. 2).

SO SEQUENCE 364 AA; 41119 MW; B0FA6265A688B7 CRC64;

Query Match 51.2%; Score 946.5; DB 1; Length 364;

Best Local Similarity 51.9%; Pred. No. 44e-60;

Matches 176; Conservative 75; Mismatches 75; Indels 13; Gaps 5;

QY 1 MNE--CHYDKHMDFFYNSNTDTVDW--TGTKLIVLVLCGFFPCFFFSNLTAAVTK 57

DB 19 MNEOCGFNESTAFYNSGKLTATENTVSKLVGL--GTYCYFIAMLANLTAAVATV 76

QY 58 NKRHFPPYYLIANAADFFAGIAYVFLMFTGVSSTLVNRFRLROGLDSSLTASL 117

DB 77 NKRHFPPYYLIANAADFFAGIAYVFLMFTGVSSTLVNRFRLROGLDSSLTASV 136

QY 118 TNLVIAVERHMSIMRMVHSLTKKRYTLILLWALAIIFGAVPTGLMNCISACS 177

DB 137 ANLAIATERHTVERMQLHTFMSNRVVVIVITWTAIVGALIPSGVNCICIDHCS 196

QY 178 SLAPYSRSLVFWFTVSNLMAFLIMVYVIRYVKRKNVLSPTSGSISRRRTPKL 237

DB 197 NMAPLXDSLYLFWALFNLVTYVAVVAVVIAHIFGYRQRTMMSHSSPPRRNRTMSL 256

QY 238 KRTVTVIGAFVYVCTPGILVPLDGLNCRQGVQVHKRWFLLALLNSVNPITYSKD 297

DB 257 LKTVVTVIGAFVYVCTPGILVPLDGLNCRQGVQVHKRWFLLALLNSVNPITYSKD 315

QY 298 EDMGTMKMKICFQENP-----ERRSPITPTVLS 329

DB 316 KEMSAFPOILCCQRNENPCTEGSDNSASSLNTTLA 354

RESULT 8

ID EDG2\_SHEEP STANDARD; PRT; 393 AA.

AC P46628;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1).

GN EDG2 OR EDG-2.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI\_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=plutitary pars tuberalis;

RX MEDLINE=96430916; PubMed=8833998;

RA Masana M.I., Brown R.C., Pu H., Gurney M.E., Dubocovich M.L.;

RT Cloning and characterization of a new member of the G-protein coupled receptor EDG family.

RT Recept. Channels 3:255-262(1995).

RL -1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of diverse cellular activities. Seems to be coupled to the G(11)/G(0), G(12)/G(13), and G(4) families of heteromeric G proteins (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: U18405; AAB52368.1; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR InterPro: IPR004065; LPARreceptor.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_RHODOPSIN.

DR PRINTS: PR01527; LPARRECEPTOR.

DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.

DR PROSITE: PS0262; G-PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Lipoprotein; Palmitate.

FT TRANSMEM 51 75 1 (POTENTIAL).

FT TRANSMEM 76 82 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 83 111 2 (POTENTIAL).

FT TRANSMEM 112 125 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 126 144 3 (POTENTIAL).

FT TRANSMEM 145 163 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 164 189 4 (POTENTIAL).

FT TRANSMEM 190 205 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 226 5 (POTENTIAL).

FT TRANSMEM 227 258 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 259 280 6 (POTENTIAL).

FT	DOMAIN	281	294	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	295	315	7 (POTENTIAL).
FT	DOMAIN	316	393	CYTOPLASMIC (POTENTIAL).
FT	LIPID	327	327	PALMITATE (BY SIMILARITY).
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	35	35	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	393 AA;	44433 MM;	356E961153C345FC CRC64;
Query Match		50.5%;	Score 932.5;	DB 1; Length 393;
Best Local Similarity		50.7%;	Pred. No. 4.6e-59;	
Matches	172;	Conservative	78;	Mismatches 76; Indels 13; Gaps 5;
QY	1 MNE--CHYDKHMEFFYNSNTDTVDW--TGTSLYIVLCVGTFFCLFFPFSNLYAAYIK	57		
Db	19 MNEQCFYNESIAEFFYNSRGKYLATEWNTVSKLVGL--GIVTCIFIMLANLVAVIYV	76		
OY	58 NRKHPEPYVLLANLAADFAGIAYVPLMNTGVSSTLVNRRNPLAQGLDLSLTSL	117		
Db	77 NRHPEFYIYMANLAADFFAGIAYFYLMTNGPNTRLRLTWLLRQGLDITVTYASV	136		
OY	118 TNLIVIVERHMSITMRHSHNLTKRPVTLILLVMAIFMGAVPTLGMCLNISACS	177		
Db	137 ANLAIAIEERIIITYFRMQLTRMSRRVVYIVIMAIYMGALPSYGMNCIDIEICS	196		
OY	178 SLAPITRSYIVETVTSKMLAPLIMVVYLRIVYKKNIVLSPHISGISRRRTPKL	237		
Db	197 NMALPSDSYSLVFAIFMLVTFEVMVLYAHIFGVRRQRTKMSHSGPRNRDPTMSL	256		
OY	238 MKYVIVGVAFVVCMTPLVVLPLDGLMCRQCGVOHVRFWFLALLNSVNPPIITYKD	297		
Db	257 LKTYIVYVGAIIICHTPGLVLLLD--VCCPCQDYLATKFFLLIAEFNSANNPITYSRD	315		
OY	298 EDMTGVMAKMKICFSGQEN-----PERRPSRIDPSTVIS	329		
Db	316 KEMSATFROIILCCORSENTSGPTSGDSASASLMTIILA	354		
RESULT 9				
EDG2_BOVIN				
ID	EDG2_BOVIN	STANDARD:	PRT;	364 AA.
AC	Q28031;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Lysophosphatidic acid receptor Edg-2 (LPA receptor 1) (LPA-1)			
DE	(Recl.3).			
GN	Edg2.			
OS	Bos taurus (Bovine).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OS	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RX	MEDLINE=97165887; PubMed=9013780;			
RA	Macrae A.D., Piemont R.T., Jaber M., Petersen A.S., Lefkowitz R.J.;			
RT	"Cloning, characterization, and chromosomal localization of recl.3, a			
RT	member of the G-protein-coupled receptor family highly expressed in			
RL	brain. "			
RL	Brain Res. Mol. Brain Res. 42:245-254(1996).			
CC	-1- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of			
CC	diverse cellular activities. Seems to be coupled to the G(i)/G(0),			
CC	G(12)/G(13), and G(q) families of heteromeric G proteins (by			
CC	similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

[illegible]

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A., AND VARIANT OVARIAN CARCINOMA.  
RC TISSUE-Ovarian carcinoma;  
RX MEDLINE=98192573; PubMed=9525886;  
RA An S., Bleu T., Hallmark O.G., Goetzl E.J.;  
RT "Characterization of a novel subtype of human G protein-coupled  
RL receptor for lysophosphatidic acid".  
RN J. Biol. Chem. 273:7906-7910(1998).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20382744; PubMed=10922489;  
RA Bandon K., Aoki J., Taira A., Tsujimoto M., Arai H., Inoue K.;  
RT "Lysophosphatidic acid (LPA) receptors of the EGF family are  
RL differentially activated by LPA species. Structure-activity  
RN relationship of cloned LPA receptors".  
RP FEBS Lett. 478:159-165(2000).  
[3]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Colon cancer;  
RA An S.;  
RT "Human Egd4 lysophosphatidic acid receptor cDNA encoding a putative  
RL protein with COOH-terminus different from the previously-reported  
RN Egd4".  
RP Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
[4]  
RP SEQUENCE FROM N.A.  
RX Lamerion J.E., McCreedy P.M., Adamson A.W., Burkhardt-Schultz K.,  
RA Garcia E., Kyle A., Ramirez M., Stllwage S., Garmes J., Dangann L.,  
RC Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,  
RN Carrano A.V.,  
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Lung;  
RA STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RC Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RN Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RN Diachenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casaventi T.L., Scheetz T.E.,  
RC Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RN Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RN Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RC Feibey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RN Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RN Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RC Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RN human and mouse cDNA sequences".  
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[6]  
RP REVIEW.  
RX MEDLINE=20545693; PubMed=11093753;  
RA Contos J.J.A., Ishii I., Chun J.;  
RT "Lysophosphatidic acid receptors".  
RN Mol. Pharmacol. 58:1188-1196(2000).  
[7]  
RP IDENTIFICATION OF A PROBABLE FRAMESHIFT MUTATION.  
RX MEDLINE=20195626; PubMed=10729222;  
RA Contos J.J.A., Chun J.;  
RT "Genomic characterization of the lysophosphatidic acid receptor gene,  
RN lp(A2)/Egd4, and identification of a frameshift mutation in a  
CC Genomics 64:155-169(2000).  
-!- FUNCTION: Receptor for lysophosphatidic acid (LPA), a mediator of  
diverse cellular activities. Seems to be coupled to the G(1)/G(0)

```
CC G(1/G(13), and G(q) families of heteromeric G proteins.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed most abundantly in testes and peripheral blood leukocytes with less expression in pancreas, spleen, thymus and prostate. Little or no expression in heart, brain, placenta, lung, liver, skeletal muscle, kidney, ovary, small intestine, or colon.
CC -1- MISCELLANEOUS: Ref.1 cDNA clone has a guanine nucleotide deletion that causes a frameshift near its C-terminal coding region. This likely reflects a somatic mutation in the ovary tumor cells from which the cDNA was isolated and may have altered the function of the encoded receptor, and contributed to transformation of the original ovary cells that formed a tumor.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC
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CC -----
CC EMBL; AF011466; AAC7728.1; ALT_FRAME.
CC DR EMBL; AF233092; AAF3409.1; -.
CC DR EMBL; AF197929; AAG28521.1; -.
CC DR EMBL; AC002306; AAB61528.1; -.
CC DR EMBL; BC025695; AAH25695.1; -.
CC DR Genew; HGNC:3168; EDG4.
CC MIM; 605110; -.
CC DR InterPro; IPR004066; EDG4receptor.
CC DR InterPro; IPR000276; GPCR_Rhodopsn.
CC DR InterPro; IPR004065; LPARreceptor.
CC Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PRO1528; EDG4RECEPTOR.
CC DR PRINTS; PR00037; GPCRRHODOPSN.
CC DR PRINTS; PRO1527; LPARRECEPTOR.
CC DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 34 54 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 70 90 2 (POTENTIAL).
FT DOMAIN 91 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 104 126 3 (POTENTIAL).
FT DOMAIN 127 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 147 167 4 (POTENTIAL).
FT DOMAIN 168 188 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 189 209 5 (POTENTIAL).
FT DOMAIN 210 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMM 243 263 6 (POTENTIAL).
FT DOMAIN 264 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMM 280 297 7 (POTENTIAL).
FT DOMAIN 298 351 CYTOPLASMIC (POTENTIAL).
FT LIPID 311 311 PALMITATE (BY SIMILARITY).
FT CARBOHYD 10 N-LINKED (GLCNAc...) (POTENTIAL).
FT CARBOHYD 18 N-LINKED (GLCNAc...) (POTENTIAL).
FT CONFLICT 221 R -> S (IN REF. 3).
SO SEQUENCE 351 AA; 39084 MW; DE235B0B3E9351B8 CRC64;

Query Match 45.6%; Score 843.5; DB 1; Length 351;
Best Local Similarity 50.3%; Pred. No. 8e-53;
Matches 156; Conservative 60; Mismatches 93; Indels 1; Gaps 1

Oy 1 MNECHYDKHMPFFNRSTWTFVDVDTGKLYIVLCVGTFECLEFFFSNSLVIAAVIKNRK 60
Db 4 MGOCYYNTTGIEFFYNSSKEKLSMHR-PKDVVVAVALGTGVSYVLITNLVIAAASNR 62
Oy 61 FHPFYYVLAAILAAADFAAGIAYAYLTMTSPVSKTLTVNNRMELOGLDDSTASTLNLT 120
Db 63 FHQPIYLLGNILAADDFAGSAVAFLTMHTGEGRTARRSLSEGFELKQGLDYSIVASVMTL 122
```





CC and embryonic brain. Other organs also express the transcript,  
 CC including heart, lung, spleen, thymus, stomach, and adult brain.  
 CC Several have little or no expression, including liver, small  
 CC intestine, and skeletal muscle.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL: AF218844; AAF65684.1; -  
 CC MGD: MGI:1858422; Edg4.  
 CC InterPro: IPR004066; GPCR\_Rhodopsn.  
 CC InterPro: IPR004065; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR01528; EDG4RECEPTOR.  
 CC PRINTS: PR00237; GPCR\_RHODOPSIN.  
 CC PRINTS: PR01527; LPARRECEPTOR.  
 CC PROSITE: PS00237; G-PROTEIN\_REC\_P1\_1; FALSE\_NEG.  
 CC PROSITE: PS50262; G-PROTEIN\_REC\_P1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Multigene family; Lipoprotein; Palmitate.  
 CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 51 51 1 (POTENTIAL).  
 CC TRANSMEM 52 66 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 67 87 2 (POTENTIAL).  
 CC TRANSMEM 88 104 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 105 124 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 125 144 4 (POTENTIAL).  
 CC TRANSMEM 145 165 5 (POTENTIAL).  
 CC TRANSMEM 166 185 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 186 206 5 (POTENTIAL).  
 CC TRANSMEM 207 239 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 240 260 6 (POTENTIAL).  
 CC TRANSMEM 261 290 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 271 291 7 (POTENTIAL).  
 CC TRANSMEM 292 348 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 308 308 PALMITATE (BY SIMILARITY).  
 CC TRANSMEM 7 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC TRANSMEM 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC TRANSMEM 348 AA; 38776 MW; E3594382D616052C CRC64;  
 CC SEQUENCE

Query Match 39.9%; Score 736.5; DB 1; Length 348;  
 Best Local Similarity 42.6%; Freq. No. 2.8e-45;  
 Matches 147; Conservative 68; Mismatches 105; Indels 25; Gaps 4;

CC 1 MNECHYKDMDFNRSTDTVDWTKLVIVLCVGFCEGLTFEFSNIVIAVYKRRK 60  
 CC 1 MGCCYNTNTTGFNNNSKELSLHR-PKDYVVAALGLTVSLVLLMLVIAALASNR 59  
 CC 61 FHPFYYLLANLAADFFAGIAYVFLMNTGSPVSKTLVNWFLROGLD----- 110  
 CC 60 FHPYLYLLGNLAADFFAGIAYVFLMNTGSPVSKTLVNWFLROGLD----- 113  
 CC 111 --SILFASLNLVIAVERHNSIMARVHNSLTKKRWLLILLVAIAIFGAVFTLGMN 168  
 CC 114 GVSCHTAG-----IAVERHNSVAVVOLHSRLPRGRVYTLIVGWAALGLGLPAHWH 167  
 CC 169 CLCNISACSLAPISRYLFWYNSLMAFLIMVYVYLYVYVYKRTNLSPTSGSI 228  
 CC 168 CLCLIDSCSRVPLFSNSYLLAALSLVFLVLAAYVTRIFPKRVERAEVNSCHP 227  
 CC 229 SRRRTPMKMTVTVLGAFFVWCWTPGLVPLDGLNRCOGVOYHKKWFLTLALNSV 288  
 CC 228 RYRETTLSLVKTVVILIGAFVWCWTPGOVVLIDGLDKTCNVLAVERYFLLAANSLV 287  
 CC 289 NPILSYDEDMYGMKMKKICFSGDENRRPRSRIPSTVLSRSDT 333

DB 288 NAVVYSCRDAMERTFRLLCCMCLRWSSHSARSASATGCAST 332

RESULT 13  
 EDGL\_MOUSE  
 ID EDGL\_MOUSE STANDARD: PRT; 382 AA.  
 AC 008530;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-1998 (Rel. 35, Last annotation update)  
 DE Probable G protein-coupled receptor EDG-1.  
 GN EDG1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE=liver;  
 RX MEDLINE=97369927; PubMed=9226368;  
 RA Liu C.H., Hla T.;  
 RT "The mouse gene for the inducible G-protein-coupled receptor edg-1.";  
 RL Genomics 43:15-24(1997).  
 CC -1- FUNCTION: THIS INDUCIBLE EPITHELIAL CELL G-PROTEIN-COUPLED  
 CC RECEPTOR MAY BE INVOLVED IN THE PROCESSES THAT REGULATE THE  
 CC DIFFERENTIATION OF ENDOTHELIAL CELLS (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES  
 CC WITH HIGHEST LEVELS IN BRAIN, SPLEEN AND HEART. LOWER LEVELS  
 CC FOUND IN LUNG, PLACENTA, MUSCLE, LIVER, UTERUS AND KIDNEY. VERY  
 CC LOW LEVELS IN TESTIS AND THYMUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC -----  
 CC EMBL: U40811; AAC53294.1; -  
 CC MGD: MGI:1096355; Edg1.  
 CC GO: GO:0007193; P:G-protein signaling, adenylate cyclase inh. .; IDA.  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC InterPro: IPR004061; S1PRECEPTOR.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCR\_RHODOPSIN.  
 CC PRINTS: PR01523; S1PRECEPTOR.  
 CC PROSITE: PS00237; G-PROTEIN\_REC\_P1\_1; 1.  
 CC PROSITE: PS50262; G-PROTEIN\_REC\_P1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Phosphorylation; Lipoprotein; Palmitate.  
 CC DOMAIN 1 46 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 47 71 1 (POTENTIAL).  
 CC TRANSMEM 72 78 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 79 107 2 (POTENTIAL).  
 CC TRANSMEM 108 121 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 122 140 3 (POTENTIAL).  
 CC TRANSMEM 141 159 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 160 185 4 (POTENTIAL).  
 CC TRANSMEM 186 201 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 202 222 5 (POTENTIAL).  
 CC TRANSMEM 223 256 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 257 278 6 (POTENTIAL).  
 CC TRANSMEM 279 294 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 295 315 7 (POTENTIAL).  
 CC TRANSMEM 316 382 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC CARBOHYD 328 328 PALMITATE (BY SIMILARITY).  
 CC LIPID 328 353 PHOSPHORYLATION (POTENTIAL).  
 CC MOD\_RES 353 353  
 CC SEQUENCE 382 AA; 42571 MW; A0048993491C8957 CRC64;

Query Match 29.58; Score 546; DB 1; Length 382;  
 Best Local Similarity 34.18; Pred. No. 8.5e-32;  
 Matches 117; Conservative 79; Mismatches 125; Indels 22; Gaps 8;

27 GFKLVYLCVGTFFCFEFSNSLYIAVAKNRKPEPFYLLANLAADFPFGIAVFL 86  
 44 GIKLTSVFL--LICCFILLENFVLLTKTKFHPMTYFGNLAISDLGAVATAN 101  
 87 MENTGPVSKTLVYRNRFRLROGLDSSLTASLTNLYAVRHMSIMRVRHNSLTKRVT 146  
 102 LLISGATYKLTPOAOWFLREGSMFVALASVFSLLAIIRYITLTKMKLHNSNSRSF 161  
 147 LLLILWALIFGAVPTLGMNCLINISACSLAPIYSRYLVFWTVSNIMAFILMVYV 206  
 162 LLISACWVSLILIGLPSMGMCNCSISLSCSTVPLTHKHYIFCTVFTLLLSITVLY 221  
 207 LRIYVYVKKRTNVLSPT--TSGSISRRTPMKLMKTVMTVLGAFVYCWTFGLVYLPD- 262  
 222 CRISLVTRTSRRRLTRKKNISKRSRSEKS-LALIKTVIIVLSVFIACMAPFLILLDV 280  
 263 GLNCRGCGVOHVRWFLLLALLNSVNPPIIYSYKDEDMYGMKMICFSQENPE----- 317  
 281 GCKAKCDILYKAEYFLVALVNSGTNPILYITLTKEMRAFAIRIVSCCKCPNDSAGKF 340

318 RRSRIPSTVLSR--SDTGSQYIEDS-----ISGAVCNKS 351  
 341 KRP1-IPGMEFSRKSNDSSHPKDDGDPETIMSSGNVSSS 382

RESULT 14  
 EDG3\_RAT STANDARD; PRT; 383 AA.

AC P48303;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-1998 (Rel. 36, Last annotation update)  
 DE Probable G protein-coupled receptor EDG-1.  
 GN EDG1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RX MEDLINE=95047498; PubMed=7959012;  
 RA Lado D.C., Browe C.S., Gaaskin A.A., Borden J.M., MacLennan A.J.;  
 RT "Cloning of the rat edg-1 immediate-early gene: expression pattern  
 suggests diverse functions.";  
 Gene 149:331-336(1994).  
 CC -1- FUNCTION: IT IS POSSIBLE THAT IT ACTS AS A RECEPTOR FOR A TROPHIC  
 FACTOR AND IS INVOLVED IN THE SURVIVAL OF BRAIN CELLS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT EMBRYONIC DAY 15, AT  
 POSTNATAL DAY 14 DETECTED IN SKIN, SPLEEN, LIVER, KIDNEY, HEART,  
 TESTICLE, LUNG AND BRAIN. AT ADULTHOOD IS MOST ABUNDANT IN BRAIN.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: U10303; AAA83418.1; -  
 CC PIR: I53870; I53870.  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC InterPro: IPR004061; 7tm\_1; 1.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHHODOPS.  
 CC PRINTS: PR01523; S1PRRECEPTOR.

DR PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Phosphorylation; Lipo-protein; Palmitate.  
 FT DOMAIN 1 47  
 FT TRANSSEM 48 72  
 FT DOMAIN 73 79  
 FT TRANSSEM 80 108  
 FT DOMAIN 109 122  
 FT TRANSSEM 123 141  
 FT DOMAIN 142 160  
 FT TRANSSEM 161 186  
 FT DOMAIN 187 202  
 FT TRANSSEM 203 223  
 FT DOMAIN 224 257  
 FT TRANSSEM 258 279  
 FT DOMAIN 280 295  
 FT TRANSSEM 296 316  
 FT DOMAIN 317 383  
 FT CARBOHYD 31 31  
 FT LIPID 329 329  
 FT MOD\_RES 354 354  
 SQ SEQUENCE 383 AA; 42745 MM; 090B6AE0DB4F3 CRC64;

Query Match 29.38; Score 541; DB 1; Length 383;  
 Best Local Similarity 34.28; Pred. No. 1.9e-31;  
 Matches 117; Conservative 77; Mismatches 128; Indels 20; Gaps 7;

27 GFKLVYLCVGTFFCFEFSNSLYIAVAKNRKPEPFYLLANLAADFPFGIAVFL 86  
 45 GIKLTSVFL--LICCFILLENFVLLTKTKFHPMTYFGNLAISDLGAVATAN 102  
 87 MENTGPVSKTLVYRNRFRLROGLDSSLTASLTNLYAVRHMSIMRVRHNSLTKRVT 146  
 103 LLISGATYKLTPOAOWFLREGSMFVALASVFSLLAIIRYITLTKMKLHNSNSRSF 162  
 147 LLLILWALIFGAVPTLGMNCLINISACSLAPIYSRYLVFWTVSNIMAFILMVYV 206  
 163 LLISACWVSLILIGLPSMGMCNCSISLSCSTVPLTHKHYIFCTVFTLLLSITVLY 222  
 207 LRIYVYVKKRTNVLSPTSGSISRRT--PMKLMKTVMTVLGAFVYCWTFGLVYLPD-G 263  
 223 CRISLVTRTSRRRLTRKKNISKRSRSEKSLALIKTVIIVLSVFIACMAPFLILLDV 282  
 264 LNCRCGVOHVRWFLLLALLNSVNPPIIYSYKDEDMYGMKMICFSQENPE-----R 318  
 283 CKAKTCDILYKAEYFLVALVNSGTNPILYITLTKEMRAFAIRIVSCCKCPNDSAGKF 342  
 319 RPSRIPSTVLSR--SDTGSQYIEDS-----ISGAVCNKS 351  
 343 RPI-IPGMEFSRKSNDSSHPKDDGDPETIMSSGNVSSS 383

RESULT 15  
 EDG3\_HUMAN STANDARD; PRT; 378 AA.

AC Q99500;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lysosphingolipid receptor (EDG-3).  
 GN EDG3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=97032811; PubMed=8878560;  
 RA Yamauchi F., Tokuda M., Hatake O., Brenner S.;  
 RT "Molecular cloning of the novel human G protein-coupled receptor  
 (GPCR) gene mapped on chromosome 9.";





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